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(54) Title: NUCLEAR ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

(57) Abstract: The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

FIELD OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides and in particular to
5 the identification of human single nucleotide polymorphisms based on at least one gene product that was not previously described.

BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been
10 widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

Several different types of polymorphisms in nucleic acid have been described. One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPs can
15 create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is in an alteration the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences
20 typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be
25 referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by

another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at 5 which one allele bears a gap with respect to a single nucleotide in another allele. Some SNPs occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, 10 e.g., genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the 15 genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of single nucleotide polymorphisms (SNPs) in regions of human DNA.

20 Accordingly, in one aspect, the invention provides nucleic acid sequences comprising nucleic acid segments of both publicly known and novel genes, including the polymorphic site. The segments can be DNA or RNA, and can be single- or double-stranded. Preferred segments include a biallelic polymorphic site.

25 The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in Table 1, column 4, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in Table 1, column 4, in which the polymorphic site within the sequence is occupied by a base other than the reference bases shown in Table 1, columns 5 and 6.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in Table 1. Optionally, a set of bases occupying a set of polymorphic sites shown in Table 1 is determined. This type of analysis can be performed on a number of individuals, 5 who are tested for the presence of a disease phenotype.

In another aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, e.g., a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long 10 as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of these sequences, or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The polynucleotide can be, e.g., DNA or RNA, and can be between about 10 and 15 about 100 nucleotides, e.g., 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

In preferred embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, e.g., the polymorphic site includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

20 In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, e.g., the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

25 In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to angiopoietin, 4-hydroxybutyrate dehydrogenase, or any of the other proteins identified in Table 1, column 10.

30 In another aspect, the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic

sequences recited in Table 1, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the

- 5 polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences in Table 1, provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the
- 10 fragment includes a polymorphic site in the polymorphic sequence.

In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, e.g., (a) a nucleotide sequence comprising one or more polymorphic sequences in Table 1, wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the

- 15 polymorphic sequence; (b) a nucleotide sequence that is a fragment of any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences disclosed herein in Table 1; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

- 20 The oligonucleotide can be, e.g., between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

- The invention also provides a method of detecting a polymorphic site in a nucleic acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected shown in Table 1, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the
- 25 oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.
 - 30

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

5 The oligonucleotide can be, e.g., between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

10 In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a nucleic acid encoding polypeptide related to one of the protein families disclosed herein. the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to angiopoietin, 4-hydroxybutyrate dehydrogenase; or any of the other proteins identified in Table 1, column 10.

15 In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected disclosed in Table 1, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids 20 to the nucleic acid indicates the first and second subjects are related.

25 In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 column for the polymorphic sequence.

The oligonucleotide can be, e.g., between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from a child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the method includes determining if a sequence polymorphism is present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence disclosed in Table 1, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences in Table 1, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, e.g., related to one of the protein families disclosed herein. For example, polypeptide can be related to angiopoietin, 4-hydroxybutyrate dehydrogenase, ATP-dependent RNA helicase, MHC Class I histocompatibility antigen, or phosphoglycerate kinase.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

5 In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

10 The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide including one or more of the polymorphic sequences in Table 1, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

15 In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

20 The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the 25 complexes indicates the presence of the polypeptide.

The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, e.g., a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology 30 associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence

shown in Table 1, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively

- 5 different polypeptides can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene.
- 10 Finally, aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence

15 comprises a polymorphic sequence which includes nucleotide listed in Table 1, column 5 for the polymorphic sequence.

Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising polymorphic sequence shown in Table 1, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of the polymorphic sequences,

20 provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence shown in Table 1, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of the polymorphic sequences, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence,

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences shown in Table 1; a nucleotide sequence that is a fragment of any of the nucleotide sequence, provided that the fragment includes a

polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more of the polymorphic sequences; or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

- 5 In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, e.g., polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, e.g., a nucleotide sequence which 10 includes one or more of the polymorphic sequences shown in Table 1, and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences, or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic 15 site in the polymorphic sequence.

Alternatively, or in addition, the kit can include the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences shown in Table 1, provided that the polymorphic sequence 20 includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences shown in 25 Table 1, provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 6. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

BRIEF DESCRIPTION OF THE DRAWING

FIG. 1 illustrates an example of the way in which SNP sites were identified in the present invention.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. Many SNPs have been identified in genes related to polypeptides of known function. If desired, SNPs associated with various polypeptides can be used together. For example, SNPs can be grouped according to whether they are derived from a nucleic acid encoding a polypeptide related to particular protein family or involved in a particular function.

Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc. Specifically, the present invention provides a large number of human cSNP's based on at least one gene product that has not been previously identified. In contrast, and as defined specifically in the following paragraph, the cSNP's involve nucleic acid sequences that are assembled from at least one known sequence.

The present invention describes 651 distinct polymorphic sites, which are summarized in Table 1. Raw traces underlying sequence data were drawn from public databases and from the proprietary database of the Assignee of the present invention. The sequences were obtained by calling the bases from these traces, and included assigning "Phred" quality scores

for each called base. For each allelic set, at the polynucleotide level, four or more nucleotide sequences were identified having at least partial overlap with one another.

- As illustrated in FIG. 1, these four or more sequences could be clustered and assembled to make a consensus contig that included an ORF. In this way, the inventors
- 5 found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by a SNP at a particular polymorphic site. In order to be confirmed as a SNP site, the nucleotide change from the consensus sequence had to occur in at least two individual sequences, and had to have a "Phred" score of 23 or higher at the site of the presumed SNP. Furthermore, in a window of 5 bases on either side of the SNP, no more than
- 10 50% mismatching with the consensus sequence was allowed. In the assembly leading to each of the contigs defining the allelic set, the SNP alleles occur in polynucleotides found in public databases.

It was found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by an SNP at a particular polymorphic site. These associations

15 were not previously known.

At the level of translation of an ORF contained in the contigs, allelic sets were identified in which one allele defines a known polypeptide sequence that includes the polymorphic site and another polypeptide allele is not previously known. Then, various associations of alleles are possible. For example, it is possible that an allelic pair is defined

20 in a noncoding region of the contig containing an ORF. In such cases the inventors believe that the invention resides in the recognition of the allelic pair; this association has not heretofore been made.

Alternatively, sets of allelic contigs may exist in which the polymorphic site is within an ORF, but does not result in an amino acid change among the allelic polypeptides. Thus, in

25 another embodiment, the polymorphic site resides within an ORF and results in an amino acid change, or a frameshift, among the alleles of the allelic set. In the sets of gene products that fall within this group, at least one of the alleles at the polypeptide level is a known protein. At least one of the remaining allele or alleles in the set, carrying a variant amino acid at the polymorphic site, is a novel polypeptide not heretofore known. The invention resides

30 at least in the recognition of the polymorphic allele as being a variant of the known reference polypeptide.

- Table 1 provides information concerning the allelic sequences. One of the sequences may be termed a reference polymorphic sequence, and the corresponding second sequence includes the variant SNP at the polymorphic site. Since the reference polypeptide sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele, while its SEQ ID NO is provided in the Table. A reference to the SEQ ID NO that corresponds to the translated amino acid sequence is also given. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and a description of each, are given below.
- 10 SNPs disclosed in Table 1 were detected by aligning large numbers of sequences from genetically diverse sources of publicly available mRNA libraries (Clontech). Software designed specifically to look for multiple examples of variant bases differing from a consensus sequence was created and deployed. A criteria of a minimum of 2 occurrences of a sequence differing from the consensus in high quality sequence reads was used to identify an 15 SNP.

The SNPs described herein may be useful in diagnostic kits, for DNA arrays on chips and for other uses that involve hybridization of the SNP.

- Specific SNPs may have utility where a disease has already been associated with that gene. Examples of possible disease correlations between the claimed SNPs with members of 20 the genes of each classification are listed below:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

25 Amyloid

- The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called 30 amyloidosis, which affects the liver, kidney and spleen and which is characterized by the

highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. Amyloid deposition is also associated with type II diabetes mellitus.

5 **Angiopoietin**

Members of the angiopoietin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various 10 antihypertensive drugs and chemotherapeutic and anti-tumor agents.

15 **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding 20 their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of antiaging drugs.

25 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and 30 anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

5 Complement-related proteins

- Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are 10 associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I 15 diabetes mellitus, meningitis neurological disorders such as Nemaline myopathy, Neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

- The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound 20 proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

- Kinesins are tubulin molecular motors that function to transport organelles within 25 cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipofuscinoses, Neuronal 1, Infantile, Santavuori disease and more.

Breakdown Classifications of SNPs

The following list describes the numerical breakdown by molecule type of the SNPs described in Table 1. The key to these molecule types is as follows.

25

	TPase_associated:	864
	Guanyl:	3
	MHC:	1077
	amylase:	44
30	amylaseinhib:	1
	amyloid:	96
	apoptosis:	91

	apoptosisinhib:	29
	apoptosisrecep:	14
	biotindep:	29
	cadhenn:	415
5	calcium_channel:	85
	carboxylase:	4
	cathepsin:	336
	cathepsininhib:	41
	chloride_channel:	90
10	collagen:	1542
	complement:	222
	complementinhib:	21
	complementrecept:	10
	csf:	31
15	csf recept:	37
	cyclin:	65
	cyto45O:	136
	cytochrome:	659
	deaminase:	44
20	dehydrogenase:	1235
	desaturase:	9
	dna_mra_bind:	1309
	dna_mra_bind_inhib:	16
	dynein:	108
25	elastase:	134
	elastaseinhib:	6
	eph:	487
	esterase:	258
	esteraseinhib:	3
30	fgf:	34
	fgf receptor:	12
	gaba:	45
	glucoamylase:	106
	glucuronidase:	14
35	glycoprotein:	3176
	helicase:	333
	histone:	272
	homeobox:	431
	hydrolase:	187
40	hydroxysteroid:	84
	hypoxanthine:	4
	immunoglob:	1106
	immunoglob_recept:	19
	interferon:	322
45	interleukin:	88
	interleukinrecept:	126
	isomerase:	404
	isomeraseinhibitor:	45
	isomeraseseceptor:	4
50	kinase:	1684

	kinase inhibitor:	187
5	kinase receptor:	233
	kinesin:	86
	laminin:	196
	lipase:	63
	metallothionein:	62
	misc_channel:	215
	ngf:	30
	nucl_recpt:	339
10	nuclease:	298
	oncogene:	783
	oxidase:	128
	oxygenase:	14
	peptidase:	150
15	peroxidase:	115
	phosphatase:	668
	phosphataseinhib:	71
	phosphorylase:	84
	polymerase:	489
20	potassium_channel:	43
	prostaglandin:	55
	protease:	954
	proteaseinhib:	271
	reductase:	243
25	ribosomal prot:	1040
	struct:	3128
	sulfotransferase:	42
	synthase:	893
	tgf:	117
30	tgfreceptor:	41
	thioesterase:	3
	thiolase:	38
	tm7:	453
	tnf:	151
35	tnfreceptor:	36
	traffic:	22
	transcripfactor:	1139
	transferase:	291
	transport:	900
40	tubulin:	334
	ubiquitin:	229
	water_channel:	18
	unclassified:	10567

The key to the molecule type is as follows:

	Abbrev:	Title:
5	amylase amylaseinhib amyloid apoptosis apoptosisinhib	amylase protein amylase inhibitor amyloid protein apoptosis associated protein apoptosis inhibitors
10	apoptosisrecep ATPase_associated biotindep cadherin calcium_channel	apoptosis receptors ATPase associated protein biotin dependent enzyme/protein cadherin protein calcium channel protein
15	carboxylase cathepsin cathepsininhib chloride_channel collagen	carboxylase protein cathepsin/carboxypeptidases cathepsin/carboxypeptidase inhibitor chloride channel protein collagen
20	complement complementrecept complementinhib csf csfrecept	complement protein complement receptor protein complement inhibitor colony stimulating factor colony stimulating factor receptor
25	cyclin cyto450 cytochrome deaminase dehydrogenase	cyclin protein cytochrome p450 protein cytochrome related protein deaminase dehydrogenase
30	desaturase dma_rna_bind dma_rna_inhib	desaturase DNA/RNA binding protein/factor DNA/RNA binding protein/factor inhibitor
35	dynein elastase elastaseinhib eph esterase esteraseinhib	dynein elastase elastase inhibitor EPH family of tyrosine kinases esterase
40	fgf fgfreceptor gaba glucoamylase glucoronidase glycoprotein	esterase inhibitor fibroblast growth factor fibroblast growth factor receptor GABA receptor glucoamylase glucuronidase glycoprotein
45	Guanylyl helicase histone HOM	guanylylate cyclase helicase histone homologous

	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
5	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
10	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
15	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
20	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
25	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
30	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor
	phosphorylase	phosphorylase
	PIR	PIR DATABASE (release 56, 29-OCT-1998)
35	polymerase	polymerase
	potassium_channel	potassium channel protein
	prostaglandin	prostaglandin
	protease	protease
	proteaseinhib	protease inhibitor
40	reductase	reductase
	ribosomalprot	ribosomal associated protein
	RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
45	SIM	similar
	SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
50	struct	structural associated protein
	sulfotransferase	sulfotransferase

	SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN	SWISS-PROT Update (release 11-NOV-98)
5	synthase	synthase
	tgf	transforming growth factor
	tgfreceptor	transforming growth factor receptor
	thioesterase	thioesterase
	thiolase	thiolase
10	tm7	seven transmembrane domain G-protein coupled receptor
	tnf	necrosis factor receptor
	traffic	tumor necrosis factor
	tnfreceptor	tumor trafficking associated protein
15	TRN	EMBL DATABASE translated entries update (20-JUL-1998)
	transcriptfactor	transcription factor
	transferase	transferase
	transport	transport protein
20	tubulin	tubulin
	ubiquitin	ubiquitin
	unclassified	Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein
25		

Table 1

A compilation of polymorphisms is listed in Table 1. Table 1 includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

- 30 The first column of the table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's sequence tag sites); <http://shgc.stanford.edu> (Stanford 35 STS's); and <http://www.tigr.org/> (TIGR STS's). The web sites also list primers for amplification of the fragments, and the genomic location of the fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the web sites concerning the fragments listed in the table is incorporated by reference in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence listed as in one of the above databases being assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This 5 base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the table lists the alternative base(s) at the polymorphic site. The fifth column of the table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the 10 table lists a 3' (downstream or reverse) primer that hybridizes with the complement of the 3' end of the sequence to be amplified. The seventh column of the table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can either be DNA or RNA. In the latter, the T's shown in the table are replaced by U's. The 15 base occupying the polymorphic site is indicated in EUT'AC-IUB ambiguity code.

“SEQ ID” provides the cross-references to the two nucleotide SEQ ID NOS: for the 15 cognate pair, which are numbered consecutively, and, as explained below, amino acid SEQ ID NOS: as well, in the Sequence Listing of the application.

Each sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label “Accession number”. The first pair of SEQ ID NOS: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic 20 acid sequence for the polymorphism. If a polymorphism carries an entry for the amino acid portion of the row, a third SEQ ID NO: appears in parentheses in the column “Amino acid before” (see below) for the reference amino acid sequence, and a fourth SEQ ID NO: appears in parentheses in the column “Amino acid after” (see below) for the polymorphic amino acid sequence . The latter SEQ ID NOS: refer to amino acid sequences giving the cognate 25 reference and polymorphic amino acid sequences that are the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one pair SEQ ID NOS: is provided, in the first column.

“CuraGen sequence ID” provides CuraGen Corporation’s accession number.

“Base pos. of SNP” gives the numerical position of the nucleotide in the nucleic acid 30 at which the cSNP is found, as identified in this invention.

“Polymorphic sequence” provides a 51-base sequence with the polymorphic site at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5’ side and the 3’ side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a “slash (/)”; and third, the polymorphic nucleotide. In certain cases the polymorphism is an insertion or a deletion. In that case, the position that is “unfilled” (i.e., the reference or the polymorphic position) is indicated by the word “gap”.

5 “Base before” provides the nucleotide present in the reference sequence at the position at which the polymorphism is found.

10 “Base after” provides the altered nucleotide at the position of the polymorphism.

“Amino acid before” provides the amino acid in the reference protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated reference amino acid sequence if the polymorphism occurs in a coding region.

15 “Amino acid after” provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO in parentheses for the translated polymorphic amino acid sequence if the polymorphism occurs in a coding region.

20 “Type of change” provides information on the nature of the polymorphism.
“SILENT-NONCODING” is used if the polymorphism occurs in a noncoding region of a nucleic acid. “SILENT-CODING” is used if the polymorphism occurs in a coding region of a nucleic acid of a nucleic acid and results in no change of amino acid in the translated polymorphic protein. “CONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are: 1) Aliphatic: Gly, Ala, Val, Leu, Ile; 2) Aromatic: Phe, Tyr, Trp; 3) Sulfur-containing: Cys, Met; 4) Aliphatic OH: Ser, Thr; 5) Basic: Lys, Arg, His; 6) Acidic: Asp, Glu, Asn, Gln; 7) Pro falls in none of the other classes; and 8) End defines a termination codon.

“NONCONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

“FRAMESHIFT” relates to an insertion or a deletion. If the frameshift occurs in a 5 coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

“Protein classification of CuraGen gene” provides a generic class into which the protein is classified. Multiple classes of proteins were identified as listed above in the discussion of Table 1.

10 “Name of protein identified following a BLASTX analysis of the CuraGen sequence” provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely.

15 “Similarity (pvalue) following a BLASTX analysis” provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of pvalue > 1 x 10⁻⁵⁰ (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel. A pvalue < 1 x 10⁻⁵⁰ defines proteins considered to be already known.

20 “Map location” provides any information available at the time of filing related to localization of a gene on a chromosome.

The polymorphisms are arranged in Table 1 in the following order:

SEQ ID NOs: 1-422 are nucleotide sequences for SNPs that are silent.

SEQ ID NOs: 423-480 are nucleotide sequences for SNPs that lead to conservative amino acid changes.

25 SEQ ID NOs: 481-619 are nucleotide sequences for SNPs that lead to nonconservative amino acid changes.

SEQ ID NOs: 620-651 are nucleotide sequences for SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic

cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

Also presented in the sequence listing filed herewith are predicted amino acid sequences encoded by the polymorphic sequences shown in Table 1.

- 5 SEQ ID NOs: 652-709 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.
- 10 SEQ ID NOs: 710-848 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.
- 15 SEQ ID NOs: 849-880 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.
- 20 Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

Identification of Individuals Carrying SNPs

Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. (1989), B. for detecting polymorphisms. See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of 10 DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, i.e., a "polymorphic protein" containing an altered amino acid at the site of translation of the nucleotide polymorphism. The cells produce the protein because they have been genetically altered by the introduction 15 of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or 20 preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical 25 chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the 30 nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other 5 in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J & 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation 10 detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide bases read from the 5' 15 end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' 20 direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence. "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by 25 a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1989)) or oligonucleotide arrays (Maskos and 30 Southern Nucl. Acids Res. 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl. Acids Res. 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res. 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl. Acids Res. 23:3944-3948 (1995), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et 26

- al. *Proc. Natl. Acad. Sci. U.S.A.* 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. *Genomics* 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. *Science* 230:1242 (1985)), chemical (Cotton et al. *Proc. Natl. w Sci. U.S.A.*, 8Z4397-4401 (1988)) or enzymatic (Youil et al. *Proc. Natl. Acad. Sci. U.S.A.*, 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer_extension (Syvanen et al. *Genomics* 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. *&&I Acids* 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. *Science* 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barany *Proc. Natl. Acad. Sci. U.S.A.*, 88:189-I 93 (1991)), gap-LCR (Abravaya et al. 5 *Nucl. Acids Res* 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., *Nucl. Acids Res*, 21:5332-5356 (1993); Thiede et al., *Nucl. Acids Res*. 24:983-984 10 (1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or 15 duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in 20 different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (Tm) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% 25 of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE 30 (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridizations.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions

depend, for example, upon a probe's length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

- A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.
- As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotides probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization. Examples of an oligonucleotide are shown in Table 1. Oligonucleotides can be all of a nucleic acid segment as represented in column 4 of Table 1; a nucleic acid sequence which comprises a nucleic acid segment

represented in column 4 of Table 1 and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 4); or a portion (fragment) of a nucleic acid segment represented in column 4 of the table which includes a polymorphic site. Preferred polymorphic sites of the invention include segments of DNA or their complements, which 5 include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of the DNA shown in the Table.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which 10 acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules 15 generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with 20 the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use 25 of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, *Tetrahedron Lett* 22:1859-1 862 (1981) and the triester method provided by Matteucci, et al., *J. Am. Chem. Soc.*, 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., *Nucleic Acids Res.* 12:61596168 (1984). Purification of oligonucleotides may 30 be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., *J. Chrom.*, 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand

using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

5 The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be
can be obtained using either the dideoxy chain termination method or the Maxam-Gilbert
method (see Sambrook et al., Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-
3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is
incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al."
10 ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York).
Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in
length, and may range upwards of 18 nucleotides in length to greater than 100 or more
consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules
15 that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-
containing nucleotide sequences of the invention, or fragments, analogs or derivatives
thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary
to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a
double-stranded cDNA molecule or complementary to an mRNA sequence. In specific
20 aspects, antisense nucleic acid molecules are provided that comprise a sequence
complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire
SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding
region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term
25 "coding region" refers to the region of the nucleotide sequence comprising codons which are
translated into amino acid. In another embodiment, the antisense nucleic acid molecule is
antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the
invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding
region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated
30 regions).

- Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as embodied herein, it is an
- 5 oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or
- 10 enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine
- 15 substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine,

20 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine,

25 pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense

30 orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or

genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in

- 5 the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed
10 on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III
15 promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641).

- 20 The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window",
25 "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window
30 may, for example, be conducted by the local homology algorithm of Smith and Waterman *Adv. Appl. Math.* 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson and

Lipman Proc. Natl. Acad. Sci. U.S.A. 85:2444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

5 Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook et al., The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The
10 nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or
15 sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic
20 polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assay of genomic DNA, virtually any biological convenient tissue samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair
25 can be used. Genomic DNA is typically amplified before analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before
30 application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNAase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

- The design and use of allele-specific probes for analyzing polymorphisms is described
- 5 by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO
89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA
from one individual but do not hybridize to the corresponding segment from another
individual due to the presence of different polymorphic forms in the respective segments
from the two individuals. Hybridization conditions should be sufficiently stringent that there
10 is a significant difference in hybridization intensity between alleles, and preferably an
essentially binary response, whereby a probe hybridizes to only one of the alleles. Some
probes are designed to hybridize to a segment of target DNA such that the polymorphic site
aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7,
8 or 9 position) of the probe. This design of probe achieves good discrimination in
15 hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect
match to a reference form of a target sequence and the other member showing a perfect match
to a variant form. Several pairs of probes can then be immobilized on the same support for
simultaneous analysis of multiple polymorphisms within the same target sequence.

- 20 The polymorphisms can also be identified by hybridization to nucleic acid arrays,
some examples of which are described in published PCT application WO 95/11995. WO
95/11995 also describes subarrays that are optimized for detection of a variant form of a
precharacterized polymorphism. Such a subarray contains probes designed to be
complementary to a second reference sequence, which is an allelic variant of the first
25 reference sequence. The second group of probes is designed by the same principles, except
that the probes exhibit complementarity to the second reference sequence. The inclusion of
a second group (or further groups) can be particularly useful for analyzing short
subsequences of the primary reference sequence in which multiple mutations are expected to
occur within a short distance commensurate with the length of the probes (e.g., two or more
30 mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site.

- 5 Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when
10 the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be
15 identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic
20 migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification
25 products can be related to base-sequence differences between alleles of target sequences.

The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,
30 muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's

disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

- Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases,
5 inflammation, cancer, system, diseases of the nervous and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach,
10 leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

- Such correlations can be exploited in several ways. In the case of a strong correlation between a polymorphic form and a disease for which treatment is available, detection of the
15 polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting
20 such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to
25 which the patient may have increased susceptibility by virtue of variant alleles. After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

- Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
30 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these

polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual.

- 5 Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.
- 10 The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match
- 15 between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the
- 20 probability that a match of suspect and crime scene sample would occur by chance.

p(ID) is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y, the probability of each genotype in a diploid organism are (see WO
25 95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

$$\text{Both Heterozygotes: } p(AB+BA)=2xy=2x(1-x)$$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- 5 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

- 10 In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($cum\ p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$cum\ p(ID) = p(ID1)p(ID2)p(ID3)\dots p(IDn)$$

- 15 The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$cum\ p(nonID) = 1 - cum\ p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into

- 20 account together with other evidence in determining the guilt or innocence of the suspect.

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 5 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

- $p(exc)=xy(1-xy)$
- 10 where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site $p(exc)=xy(1-xy)+yz(1-yz)+xz(1-xz)+3xyz(1-xyz))$, where x, y and z are the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

- $p(non-exc)=1-p(exc)$
- 15 The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

- $cum\ p(non-exc)=p(non-exc1)p(non-exc2)p(non-exc3)\dots p(non-excn)$
- The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

20 $cum\ p(exc)=1-cum\ p(non-exc).$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

- 25 The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For

example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a 5 single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial 10 diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, 15 brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the 20 presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated 25 with the trait of interest. Correlation can be performed by standard statistical methods such as a χ^2 -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at 30 polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is

available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions.

- 5 For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.
- 10

- 15 For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect
20 to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

- The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al.,
25 *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).
- 30

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihood is usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984))). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in

excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene
5 inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of
10 a positive selection marker. See Capecchi, Science 244, 1288-1292. The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

The invention further provides methods for assessing the pharmacogenomic
15 susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic
20 characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering
25 to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

A subject suspected of suffering from a pathology ascribable to a polymorphic protein
30 that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate

polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional

components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the
5 kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences
10 complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is
15 prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. Gene 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either
20 mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, Science 196:180-182 (1977). Colony hybridization is carried
25 out as generally described in M. Grunstein et al. Proc. Natl. Acad. Sci. USA. 72:3961-3965 (1975). DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of
30 the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications

(Innis, M., Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990).

Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of protocols to isolate cDNA's encoding a sequence of interest. In these protocols, appropriate

- 5 primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It

- 10 is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a
15 sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain, initiation sequences, transcription and translation terminators, and promoters useful for regulation of the
20 expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences
25 permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a
30 strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this

purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda (P_L) as described by A, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to 5 ampicillin, tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be 10 accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or 15 immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be 20 expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of 25 replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., Gene 8:17-24 (1979); Broach, et al., Gene 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glusulase, followed by addition of 30 DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, Nature (London) 275:104-109 (1978); and Hinnen, A., et al., Proc. Natl.

Acad. Sci. USA, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., J. Bact, 153:163-168 (1983)). cells and applying standard protein isolation techniques to the lysates:.

- 5 The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells.
- 10 Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include
- 15 expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV tk promoter or pgk (phosphoglycerate kinase) promoter), an enhancer (Queen et al. *Immunol. Rev.* 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

- 20 Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and Drosophila cell lines such as a Schneider cell line (See Schneider J. *Embryol. Exp. Morphol.*, 27:353-365 (1987). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., *J. Virol.* 45: 773-781 (1983)). Additionally, gene sequences to
- 30 48

control replication in the host cell may be Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known

- 5 methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical
10 Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are
15 exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein
20 is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term "gene" as used herein is intended to refer to a nucleic acid sequence which
25 encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced
30 from the mRNA transcript, along with variants resulting from alternative splice sites.

- A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, Candida or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.
- The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.
- The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly

produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may 5 be purified to substantial purity by standard techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as 10 described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration 15 and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl@ or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity 20 chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and 25 InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP- HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be 30 employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other

mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain 5 an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and F_{(ab)2} fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically 10 immunoreactive with", an antibody when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. 15 Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, 20 solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies*, a Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

25 Polyclonal and/or monoclonal antibodies that immunospecifically bind to polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring 30 Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific

immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

- An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that bind the polymorphic protein using standard
5 techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such
10 that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the
15 surface of the protein, e.g., hydrophilic regions.

- For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation
20 can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If
25 desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

- The term "monoclonal antibody" or "monoclonal antibody composition", as used
herein, refers to a population of antibody molecules that originates from the clone of a singly
30 hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic

protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the
5 hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present
10 invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of
15 single-chain antibodies specific to a polymorphic protein (see e.g., U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can
20 be "humanized" by techniques well known in the art. See e.g., U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an F_(ab')2 fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_(ab')2 fragment; (iii) an F_{ab} fragment generated by the treatment of the
25 antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by
30 recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent
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Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 239:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeven *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,

- g a lactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a
5 luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymerase sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similarity (pValue) following a BLASTX analysis	Map location
1	cq4333349	1008	CGCTGACAGGGGA GTCTGAGCCACA /GJACCCGCTAACCC CGAGTGCAGCAC G	A	G	Gln	Gln	SILENT-CODING	ATPase associated	Human Gene SWISSPROT-ID: P220648 POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN (EC 3.6.1.36) (PROTON PUMP) (GASTRIC H+-K+-ATPASE ALPHA SUBUNIT) • HOMO SAPIENS (HUMAN), 1035 aa.	0	19
2	cq43931765	2296	ATGGATAGTCAT CTGGTGGATGCTA /TGTTGACTGTTG GCCCTGTTCAAGT	A	T	Thr	Thr	SILENT-CODING	cathepsin	Human Gene SWISSPROT-ID: P18684 INTEGRIN BETA-5 SUBUNIT PRECURSOR • HOMO SAPIENS (HUMAN), 799 aa.	0	3

3	cg4130533	1832	AATACAAAGCTGTA GTTGGAGGAGGT /GGGGTGAAGAAGCT ATGGCAATTCAAG T	G	Val	SILENT-CODING	cathefelin	Human Gene SWISSPROT-ID:PI3591 NEURAL CELL ADHESION MOLECULE, 140 KDa ISOFORM PRECURSOR (NCAM-140) (CD56 ANTIGEN) - HOMO SAPIENS (HUMAN), 848 aa
4	cg4888922	2130	TATGTTATATGTT ATTCTGTTACAG TGTTCTCTGTCA CTGCTAAAGAAA	A	G	Thr	SILENT-CODING	Human Gene SWISSPROT-ID:Q0654 DESMOCOLLIN 1A/B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2/DG3) - HOMO SAPIENS (HUMAN), 894 aa
								Human Gene SWISSPROT-ID:Q0854 DESMOCOLLIN 1A/B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2/DG3) - HOMO SAPIENS (HUMAN), 894 aa

5	cg4888922	815	CAAGGGCATATGACCGTGAGAAATAC /TGAAACATTTGC GTTATATGCCATATG	C	T	Tyr	Tyr	SILENT-CODING	cadherin	Human Gene SWISSPROT- ID:Q08354 DESMOCOLLIN 1A/IB PRECURSOR GLYCOPROTEIN (2/3) (DG2/DG3) - HOMO SAPIENS (HUMAN), 894 aa alias:SWISSPROT-ID:Q08554 DESMOCOLLIN 1A/IB PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2 / DG3) - HOMO SAPIENS (HUMAN), 894 aa.	0	18
6	cg40310734	1172	TGGCCTCCATTIT GGGCATTCAGTG/C CTGTCTCACTGAC GTCAAACGGGATG	G	C	Val	Val	SILENT-CODING	cadherin	Human Gene SWISSPROT- ID:PO8514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1B) (INTEGRIN ALPHA-1B) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
7	cg40310734	2243	AGGGGGCTATGA AGCAGAGCTGCGC /GIGTCACTTGC CCAGGGCCCCAC T	C	G	Ala	Ala	SILENT-CODING	cadherin	Human Gene SWISSPROT- ID:PO8514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1B) (INTEGRIN ALPHA-1B) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
8	cg40310734	812	GTACTGGAAAC GGGCTCACTCTC/ GTTGGTCACTCTAG GCCGGAGAGCTGG	C	G	Ser	Ser	SILENT-CODING	cadherin	Human Gene SWISSPROT- ID:PO8514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1B) (INTEGRIN ALPHA-1B) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)

9	cg43331935	1922	GTCAGAACAGTACTT CATAGGAGATGGI GTCUCUCCTGTCA CCACAGCGCTGGAC T	G	T	Gly	SILENT-CODING	cathelin	Human Gene SWISSPROT-ID:P32004 NEURAL CELL ADHESION MOLECULE LI PRECURSOR (NCAM11)- HOMO SAPIENS (HUMAN), 127 aa.	0	X
10	cg42388009	383	AAGGAGAAACAA TGAGCAACGAA CTGAAGAGAGAAG ACCTGAGCTGA GA	C	T	Asn	SILENT-CODING	cathelin	Human Gene SWISSPROT-ID:P21815 BONE SHALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SHALOPROTEIN) (INTEGRIN-BINDING SHALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7.00E-172	4
11	cg42388009	389	AAAACAAATGAGA ACCGAACAGAGA CTTGAAAGACTCTG AGGCTGAAATAC CA	C	T	Asp	SILENT-CODING	cathelin	Human Gene SWISSPROT-ID:P21815 BONE SHALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SHALOPROTEIN) (INTEGRIN-BINDING SHALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7.00E-172	4
12	cg4126574	1289	AGAACCGGGAGGC CCTGGGATTC GIGGGATGTC CTCAGGCTACT	C	G	Leu	SILENT-CODING	cathelin	Human Gene SWISSPROT-ID:Q64411 PROGASTRINSIN PRECURSOR (EC 3.4.23.3) (PEPSIN C) - CAVIA PORCELLUS (GUINEA PIG), 394 aa.	8.00E-155	6 (Op21.3)

13	cg13970983	3066	GGAATCCAGTGC CAGGGATCAG TTAACATCCATCC TGCGCGGCACTCA	C	T	Ser	SILENT-CODING	collagen	Human Gene SWISSPROT- ID:Q02388 COLLAGEN ALPHA I(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC-COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
14	cg14032748	245	TAAGACGGCAGC A	G	A	Ala	SILENT-CODING	complement	Human Gene SWISSPROT- ID:R07357 COMPLEMENT COMPONENT CS ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 364 aa.	0	1 (1p32)
15	cg1535795	222	TGACGCCAGC CAATTGATGCTT GTCAGCATTTGCA GGGACTGTGCTC	T	G	A	SILENT-CODING	complement	Human Gene Homologous to SWISSPROT-ID:R07360 COMPLEMENT C8 GAMMA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 202 aa.	1.40E-104	9 (q34.3)
16	cg13942011	1371	AAGTAGGGGCT TGTCTCCAACAA GTCCTATGTTCA TTCCTCACAGTC	A	G	Gly	SILENT-CODING	complement pr	Human Gene Similar to TRM (BLNEW-ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE)), 651 as (fragment).	1.10E-69	1 (1q32)
17	cg21644442	1219	AAACAGCCGAGA TGAACTGTGAC CGCTCTGCGAG GTTGGCCCCGTG	A	C	Thr	SILENT-CODING	csf	Human Gene SWISSPROT- ID:R09603 MACROPIPAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (M-CSF) - HOMO SAPIENS (HUMAN), 554 aa.	5.00E-304	1 (1p21)

18	cg41533258	597	TCCAGGGGGG AGAGGGTCTCTG /A/GTTGCCCTCCAT CTGCAGAGCTTC	G	A	Leu	Leu	SILENT- CODING	csf	Human Gene Homologous to SWISSPROT-ID:P09919 GRANULOCYTE COLONY- STIMULATING FACTOR PRECURSOR (G-CSF) (PLURIPOTENT - HOMO SAPIENS (HUMAN), 207 aa.	1.50E-107 (17q11.2)	17
19	cg43996714	1743	ATGTOCCACTC ATGGGTTGCTCA/ GIGGAGTTGACT GCTGGGATGACAG	A	G	Pro	Pro	SILENT- CODING	dehydrogenase	Human Gene TREMBL NEW- ID:G2979623 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR, HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266 11	11
20	cg43259523	366	CAGAAATGGGG CACAGGAGCTCA /TTTTTATCACT GTGCTCGTATAG	A	T	Ser	Ser	SILENT- CODING	dehydrogenase	Human Gene SWISSPROT- ID:PA5954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2- MBCAD) - HOMO SAPIENS (HUMAN), 452 aa.	2.00E-229 (10q5)	10

[21]	cg43057018	1528	GAATAAGA-AATTIC AACTGGATGCAJC TTGGTGACCCATA CCCTGCCCTTGTGA	C	T	Leu	SILENT-CODING	dehydrogenase	Human Gene SWISSNEW-ID:PO819 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa; SPOTREBL-ID:Q92819 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)
[22]	cg1395871	430	GIGCICCAGAGGG GCAGCAGCACI AGGGAAAACCG AAACCAACAGGA CT	A	G	Thr	SILENT-CODING	dynamin	Human Gene Homologous to SPOTREBL-ID:Q92816 CYTOPLASMIC DYNENIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103	
[23]	cg1395871	436	CAGAGGGCAGC AGGCACAGGAAA A/GAACGAAACCA CCAAGGACTGGC TA	A	G	Lys	SILENT-CODING	dynamin	Human Gene Homologous to SPOTREBL-ID:Q92816 CYTOPLASMIC DYNENIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103	
[24]	cg1395871	542	AGCAAATGGGAAG TTTTAAAGAIC TTGGCTTCCTG GTTGGCTGGCTG	C	T	Leu	SILENT-CODING	dynamin	Human Gene Homologous to SPOTREBL-ID:Q92816 CYTOPLASMIC DYNENIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103	

25	cg1395871	571	CTCTCTGGGTCT TGGCCTGCTTGT IGATGAATTCAACC GGATTTGAGTTGG	C	T	Phe	SILENT-CODING	dynamin	Human Gene Homologous to SPTRM3BL-ID:Q92816 CYTOPLASMIC DYNINEIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103		
26	cg13950268	1269	AAGGGGCCACCAT GGCCCTAGGTCIG /AATCACAGTC ACCGCAATCATG G	G	A	Asp	SILENT-CODING	epiph	Human Gene TREMBLNEW- ID:Q285466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16	
27	cg3918831	461	CCGATGGCTATGA GCAGGCTGCTGCG /TGTGCTATGAA CACCTGGACAAA	C	T	Arg	A/G	SILENT-CODING	epiph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN)- PYROCOCCUS KODAKARAENSIS, 546 aa SwissProt-ID:Q282500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN)- PYROCOCCUS SP. (STRAIN KODI), 546 aa.	1.00E-104	5

28	cg13957743	1146	CAAGTTCCTAAAT AAAATGGCCAGCTTC TTTCAGGTCTACT GGCTCCACTCTC	C	T	Glu	Glu
					SILENT- CODING	esterase	
							Human Gene SWISSNEW- ID:Q15166 SERUM
							PARAOXONASE/ARYLESTERA SE 3 (EC 3.1.1.2) (EC 3, 1.8.1) (PON-3) SERUM
							ARYLDIACYLPHOSPHATASE 3) (A-ESTERASE 3)
							(AROMATIC ESTERASE 3) HOMO SAPIENS (HUMAN), 341 aa (fragment) [db:SWISSPROT; ID:Q15166 SERUM]
							PARAOXONASE/ARYLESTERA SE 3 (EC 3.1.1.2) (EC 3, 1.8.1) (PON-3) SERUM
							ARYLDIACYLPHOSPHATASE 3) (A-ESTERASE 3)
							(AROMATIC ESTERASE 3) HOMO SAPIENS (HUMAN), 341 aa (fragment).

29	cg43319420	963	TCA CCT CAG GAG GTG GCG TGT CTC AGC TGT CCA GAC AAC TAC AGA AAG AAC	C	T	Cys	Cys	SILENT-CODING	esterase	Human Gene Similar to SWISSPROT-DB ID:Q23917 3'-5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA)- DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa; swissprot-ID:Q23917 3'-5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA)- DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3,30E-60	21
30	cg2001932	1631	TCT TCA AAC ATG GTC TAT TGG CCT TA AC T TT ATG TGA ACT AAA AC ATG GGC TCC C	C	T	Tyr	Tyr	SILENT-CODING	gaba	Human Gene SWISSPROT-ID: P17870 GAMMA-AMINOBUTYRIC-ACID RECEPTOR, BETA-2 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 474 aa.	1,90E-256	5 (5q34)
31	cg43975899	370	GGAT TTG GAC AG ACT CCT AG ATG GC /TT ATG GAC AT AGC CTG AGA CG AGG AT	C	T	Gly	Gly	SILENT-CODING	gaba	Human Gene SWISSPROT-ID: P14667 GAMMA-AMINOBUTYRIC-ACID RECEPTOR, ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1,30E-248	5 (5q34)

32	cg43299024	1643	GGGCCACTTCGC CTTGTACCTCCAA /GTTGAAACCACT T	A	G	Gln	SILENT- CODING	glucosidase	Human Gene TREMBL NEW- ID:Q2826321 MALTA SE- GLUCOMYLASE (EC 3.2.1.20) -HOMO SAPIENS (HUMAN), 1837 aa.	7.40E-199 (17q25.2)	
33	cg43299024	2021	TGAACCGAGGCTTC CAACTCTATCAGG /AAGGCTCTAGGA CGGCTCCAACAC A	G	A	Arg	SILENT- CODING	glucosidase	Human Gene TREMBL NEW- ID:Q2826321 MALTA SE- GLUCOMYLASE (EC 3.2.1.20) -HOMO SAPIENS (HUMAN), 1837 aa.	7.40E-199 (17q25.2)	
34	cg43869076	443	AATTCCAAATGAG CTCTCAACACAG /AATTTCCTGCCT TITTGATCACAC	G	A	Tyr	Tyr	SILENT- CODING	glucuronidase	Human Gene SWISSPROT- ID:PO236 BETA- GLUCURONIDASE PRECURSOR (EC 3.2.1.11) (BETA-GI) - HOMO SAPIENS (HUMAN), 651 aa.	0 (7q21.11)
35	cg43869014	325	AATTCCAGATGAG CTCTCAACACAG /AATTTCCTGCCT TITTGATCACAC	G	A	Tyr	Tyr	SILENT- CODING	glucuronidase	Human Gene Similar to SWISSPROT-ID:PO236 BETA- GLUCURONIDASE PRECURSOR (EC 3.2.1.11) (BETA-GI) - HOMO SAPIENS (HUMAN), 651 aa.	7.40E-80 5
36	cg431065549	880	GGACCATCTCTGT GGACCACTCGG /AAGACGCTGATT GGCCACTACTGC	G	A	Ala	SILENT- CODING	glycoprotein	Human Gene SWISSPROT- ID:PI6452 ERTHROCYTE MEMBRANE PROTEIN BAND 4.2 (PA2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0 (15q15)	

37	cg43065549	991	ACCCGTGAGATAG AGAGGATGTTGTTT /GTTGCTGAGAA TGAGGCTAGGCC A	T	G	Val	Val	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2(P4.2) (PALIUDINI - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
38	cg44004239	1141	TGACCTCAACAT GTCGAATGTCAC/C TJACCATGGCCCC CAAAAATGCTTC	C	T	Val	Val	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
39	cg44004239	1846	GAAGGGATAATAAC TGAAAGCAATAAAC /TTTTTACCGTTG GCAAATGTGACA	C	T	Lys	Lys	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
40	cg43957605	1677	AGGACTTTTCA TTAACGTCAGAAC /GTGATTCCATGG GCTCTCTGTGA	A	C	Thr	Thr	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P25) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)

[4]	cg46915005	1229	A/GCTCAGGATT/C TACCCAAAAGCC/C TGTTGGGGATGATG TGGATGCCGGGTO	T	Pro	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID: P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6(LEU-6) (H1A1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa) [acces:SWISSPROT-ID:P06126	2.00E-183	1 (1q21)
42	cg40356255	1210	TGGCAATAATAGT GCCTTCCTCTTC/C TCTTTCGATGATGC CTTGCAATTGTGT	C	Leu	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID: P29016 T-CELL SURFACE GLYCOPROTEIN CD1B PRECURSOR (CD1B ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa [acces:SWISSPROT-ID:P29016 T-CELL SURFACE GLYCOPROTEIN CD1B PRECURSOR (CD1B ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa]	6.70E-183	1 (1q21)

43	cg44004667	1183	CTGTGATATCTTACA TCGGGCCGCCCCCT TTGCCCGAGACTCT TGGGGTTCCTCT	C	T	Leu	SILENT-CODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T-LEU-2) - HOMO SAPIENS (HUMAN), 235 aa. (pds:SWISSPROT-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T- LYMPHOCYTE DIFFERENTIATION ANTIGEN T-LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.)	7.60E-127	
44	cg43068999	544	AGGGTCTGGGACA GGGTACTTCTTGTC AAGAAGCTCAACCC AAGATTCCTCTGG	G	A	Val	SILENT-CODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P02743 SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (5S ALPHA-1-GLYCOPROTEIN)* HOMO SAPIENS (HUMAN), 223 aa.	1.60E-119	1 (1q21)
45	cg41568631	1242	ATGGCCAACTGCTG GCCTCTTGCTGCG AATGACCAACACA GTGCTCGCTGCG	C	A	Gly	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)

46	cg41568631	1545	GCTCTGGAGTC CATCAAGAATGGC (GCTGTCTACATG AAAGTACGACACG	C	G	Gly	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ER THYROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
47	cg41603916	361	GCATCCAGTGGGT ACGGGACCTCGIC TTTGGAAAGGATGG CTCCATTGTCATACT	C	T	Arg	AAG	SILENT-CODING	Human Gene Similar to SWISSPROT-ID:Q9J406 IP1=CNS MYELIN POL-LIKE GLYCOPROTEIN - UNKNOWN, 202 aa.	3.00E-52	1 (1q22)
48	cg41603916	409	TACACAACTTACA CTACAGTCAACT CTGGCACGTTCACT TGTGACGTAAAA	T	C	Asn	Ash	SILENT-CODING	Human Gene Similar to SWISSPROT-ID:Q9J406 IP1=CNS MYELIN POL-LIKE GLYCOPROTEIN - UNKNOWN, 202 aa.	3.00E-52	1 (1q22)
49	cg43417662	465	AGTCCCTCTCCGT GGACCTTAGCTG CITATGGTTGAG AAGCCCTTGCCA	G	C	Ala	Ala	SILENT-CODING	Human Gene Homologous to SWISSPROT-ID:Q12099 PROBABLE ATP-DEPENDENT RNA HELICASE FAL-1 - SACCHAROMYCES CEREVISIAE (BAKERS YEAST), 399 aa.	3.60E-120	17
50	cg43983917	1353	AGCTTACTTGTCC ATTAAACCAAAAC TCCCCAGGCGAAC GACTGAAAGCAG	C	T	Asn	Ash	SILENT-CODING	Human Gene SWISSPROT-ID:P50458 HOMEobox PROTEIN Lhx2 - HOMO SAPIENS (HUMAN), 423 aa.	4.30E-216	

51	cg43983917	1359	ACTTGCCATTAAC CACAAACCGA/C TGGCAAAGACTTG AAGCAGCTGGC/C	C	T	Asp	SILENT-CODING	homeobox	Human Gene SWISSPROT- ID:P50458 HOMEOBOX PROTEIN Lhx-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.30E-216	
52	cg42730678	979	TGGAGGACCGTG GATCCAGTTGCCG /TGGCGGGGTGTT GGGTCAAGTGTCT	G	T	Ala	SILENT-CODING	homeobox	Human Gene SWISSPROT- ID:P23356 HOMEOBOX PROTEIN HOX-09 (HOX-4C) (HOX-5.2) - HOMO SAPIENS (HUMAN), 342 aa.	2.60E-188	2
53	cg42714160	689	GTTACCCAGACGCT GGAGCTGGAGAAC GA/GAGTTCACT ACAATGCTACCT GA	G	A	Lys	Lys	SILENT-CODING	Human Gene Homologous to SWISSPROT-ID P17599 HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2)- HOMO SAPIENS (HUMAN), 224 aa.	1.10E-123	
54	cg43959084	810	TCAAGTAGGGATT GTAGTGAATTCCTV CTTCTCACTCTCC AGGGTCCTGTAAC	T	C	Lys	Lys	SILENT-CODING	Human Gene Homologous to SWISSPROT-ID P09639 HOMEBOX PROTEIN HOX-B7 (HOX-2C) (HHO.C1) - HOMO SAPIENS (HUMAN), 217 aa.	1.30E-113	
55	cg42359555	1124	GGGAAGCATTCG CAATCACTCAGGA /GJCGGAAAGGG TCCTTCCTCAAGG	A	G	Arg	SILENT-CODING	hydrolase	Human Gene SWISSPROT- ID:P09848 LACTATE PHILORIZIN HYDROLASE PRCURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE GLYCOSYL CERAMIDASE)- HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2e21)

56	cg42359655	2468	ACAGCCAGGGGT TGCCCTGCCAAC (TGTCAAACTCA GACAGGAGCAAAT	C	T	His	SILENT- CODING	hydrolase	Human Gene SWISSPROT- ID: P09848 LACTASE- PHORLIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62 (LACTASE- GLYCOSYLCERAMIDASE)- HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2421)
57	cg42359655	4340	ATCTGGTACCCCTG CAGAACCTGGC/C TGTGTCCTAC CGTTTTCACT	C	T	Gly	SILENT- CODING	hydrolase	Human Gene SWISSPROT- ID: P09848 LACTASE- PHORLIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62 (LACTASE- GLYCOSYLCERAMIDASE)- HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2421)
58	cg43998672	1329	TGGTGTGGCCCT GGTAACACTA/GC /A/ACGGGGCTAA GTCTCCGTGTTGG	C	A	Val	SILENT- CODING	hydroxysteroid hydrolase	Human Gene SPTRMBL- ID: Q13164 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16422)
59	cg43998672	1689	GGAGGTGTACTCC AGAGGCCATGCC /TGACCTCAACTCC TCACCTGACTG	C	T	Pro	SILENT- CODING	interleukin	Human Gene TREMBLNEW- ID: G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15

60	cg42908571	630	G T A G T G A G G A A C A A G C A G A G G C G T G /C I C A G A T G A G T A C A A A A G T C C T G A T C C	G	C	Val	SILENT-CODING	Interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) -HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (P21)
61	cg43942050	181	A C T T G G A A G T G A A T G G A T G C G A G A C /T T C A C T G A C C T G T G C T T T G A G G A C C	C	T	His	SILENT-CODING	Interleukin receptor	Human Gene SWISSPROT-ID:P6871 INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA) (CDW127) (CD127 ANTIGEN) -HOMO SAPIENS (HUMAN), 459 aa http://swissprot.expasy.org/entry/P6871 INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA) (CDW127) (CD127 ANTIGEN) -HOMO SAPIENS (HUMAN), 459 aa	3.10E-249	5 (P13)

62	cg43145505	1249	TAAATATTGAGA CAATTACAGAGATC /TTATGTCCAAACA GCTATCTAACATG	C	T	Ile	SILENT-CODING	kinase	Human Gene SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHAI) (PTDNS3- KINASE P110) (PI3K) -HOMO SAPIENS (HUMAN), 1068 aa;	0	3
63	cg43918241	1693	AGATCTTGAGGA AGGGAAATGAC /TGTAGACTTGAC ATGGATGAGAAC	C	T	Asp	SILENT-CODING	kinase	Human Gene SPTRMBL- ID:Q63533 SNF1-RELATED KINASE - RATTUS NORVEGicus (RAT), 746 aa.	0	3
64	cg43090990	1438	TTCGACGCCAT GTTTGACATTC TCAGACCAAGGA AAACCTCTTTG	C	T	Phe	SILENT-CODING	kinase	Human Gene SWISSPROT- ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC2.7.1.-) (NPKC-THETAI) -HOMO SAPIENS (HUMAN), 706 aa.	0	10

65	cg43569763	2339	TGATGATCATTCAC TGCTGATCTAAAGA GICCTGAAAATATC CTCTTCTTGTAAACC	A	G	Lys	SILENT-CODING	Kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC2.7.1.-) (HP86) (DyRK) - HOMO SAPIENS (HUMAN), 763 aa.	0	21 (21q22.1)
66	cg42879455	2062	AGGATAAACATT CATATCACAGTTGT CTGGCATGAGAAA GCAGATGACGTC	T	C	Cys	SILENT-CODING	Kinase	Human Gene SWISSPROT-ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0	X (Xq21.3)
67	cg42659872	1744	TGGCTCGCGTAC ACCAACATCATGIA /CGGGTGTCAAGC ATATCCTGAAGCC	A	C	Arg	SILENT-CODING	Kinase	Human Gene SPTRMBL-ID:Q16715 PYRUVATE KINASE (EC2.7.1.40) - HOMO SAPIENS (HUMAN), 587 aa (Fragment).	9.8E-308	1 (1q21)

68	cg42506800	1323	GCTGCCAAATTCT CCTCTGATGCAC AAAGTACTTCAG GAGATCTGAATC	A	C	Ala	Ala	SILENT-CODING	kinase	ID:Q16654 [PYRUVATE DEHYDROGENASE/LIPOAMID E] KINASE ISOZYME 4 PRECURSOR (EC:2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 4) - HOMO SAPIENS (HUMAN), 411 aa[dbid:SPREMBL;ID:Q16654]	Human Gene SWISSPROT-ID:Q16654 [PYRUVATE DEHYDROGENASE/LIPOAMID E] KINASE ISOZYME 4 PRECURSOR (EC:2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 4) - HOMO SAPIENS (HUMAN), 411 aa.	1.60E-220	7 (7q21.3)
69	cg43966621	526	CCTGGGAGAACAT GTAGCTGAGAGIC TTGGCTAACATCTC CTCAAGGGACAC	C	T	Arg	Arg	SILENT-CODING	kinase	ID:Q15119 [PYRUVATE DEHYDROGENASE/LIPOAMID E] KINASE ISOZYME 2 PRECURSOR (EC:2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa[dbid:SPREMBL;ID:Q15119]	Human Gene SWISSPROT-ID:Q15119 [PYRUVATE DEHYDROGENASE/LIPOAMID E] KINASE ISOZYME 2 PRECURSOR (EC:2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.	3.80E-219	17
70	cg43917871	1448	ACAATATAATGGC CGCTGTGAGGCG /TGTAATGCCCT GGCATGCTAATG	C	T	Thr	Thr	SILENT-CODING	kinase	ID:PI19138 CASEIN KINASE II, ALPHA CHAIN (CK 1) (EC:2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	Human Gene SWISSPROT-ID:PI19138 CASEIN KINASE II, ALPHA CHAIN (CK 1) (EC:2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)

71	cg13917871	1526	CAGTGUAGAAATA GGGGTCTCTCATTT GIGCCCTCTTGCA GTAAGCGGTGACT	T	G	Ala	Ala	SILENT-CODING	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20 bp 13)
72	cg44131752	912	AGCTGAATGGGG CTCTCGTGTCTG/ AATCCGAAGTGC CTGCCCTGGTTCGG	G	A	Ser	Ser	SILENT-CODING	kinase	Human Gene SPTREMBL- ID:Q15589 TYROSINE KINASE ACTIVATOR PROTEIN 1 (KA- 1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
73	cg43969473	1765	AAITCAACCAACT CATCTATGCAATT/ CIGATGTTGAACT GTGGAATGTGCAA	T	C	Asn	Asn	SILENT-CODING	kinase	Human Gene SPTREMBL- ID:Q27467 SIMILARITY TO TYROSINE PROTEIN KINASE- CAenorhabditis elegans, 1260 aa.	2.10E-154	11
74	cg44025289	610	AGACCCGGGTC CCCTGGCAAGCTT /CGTGGAGTGCTG CCAAGGGACTGG T	T	C	Ala	Ala	SILENT-CODING	kinaseceptor	Human Gene SWISSPROT- ID:Q04771 ACTIVIN RECEPTOR TYPE I PRECURSOR (EC 2.7.1.-) (ACTR-1) (SERINE/TREONINE-PROTEIN KINASE RECEPTOR RI) (SKR1) (ACTIVIN RECEPTOR-LIKE KINASE 2) (ALK-2) (TGF-B SUPERFAMILY RECEPTOR-LIKE TYPE 1) (TSE-1) - HOMO SAPIENS (HUMAN), 509 aa.	7.90E-283	2

75	cg43318277	1107	CTCACGGTTCAG TCATCTGTCCTGAA GCCATGACCTCCCT CCTCTCTCGGC	G	A	Pro	SILENT-CODING	MHC	Human Gene SPTRMBL- ID:Q02616 MHC BINDING PROTEIN 2 - HOMO SAPIENS (HUMAN), 2500 aa.	1.20E-247	6
76	cg43966144	632	TAAACAGGGGA GCCCTGTATCTG/ AAGCTCTAATG TGGGGCTATC	G	A	Leu	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P2688 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147	6 (sp21.3)
77	cg42686558	644	CCCCCTGATCAAT ATCAGCTGGCTA/ GJGGCAACGSGCA AACTCTAACCTGAG G	A	G	Leu	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHIC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (sp21.3)
78	cg42686558	857	CACCAAGAGATGC CATGGAGACCTG /AAGCTGTGGCTG GGCCCTGGCATCG	G	A	Leu	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHIC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (sp21.3)
79	cg42686558	869	CCATGGAGACCCCT GGCTCTGTCCTG/ AAGGCTGGCAGTC GGCCCTGGTGCGCT	G	A	Leu	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHIC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (sp21.3)

80	cg42686558	881	TGGTCTGTGCCCTG GACCTGAGCATCT TGCCTGAGGGCT TCCTCGTGGCA	C	T	Ile	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II ANTIGEN, D2 ALPHA-CHAIN PRECURSOR (MHC DNA-ALPHA) -HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (sp21.3)
81	cg42686558	893	TGGGCCCTGCCAT CGGCCCTGGGGC /GTTCCCTCTGGC ACCGTCCTCATCA	C	G	Gly	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II ANTIGEN, D2 ALPHA-CHAIN PRECURSOR (MHC DNA-ALPHA) -HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (sp21.3)
82	cg42686558	905	TGGGCCCTGGGG CTTCCCTGGGCG TJACCTCTCATC ATCATGGACAT	C	T	Gly	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II ANTIGEN, D2 ALPHA-CHAIN PRECURSOR (MHC DNA-ALPHA) -HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (sp21.3)
83	cg42686553	279	GTTCCTCTATTAGC CCTGTGACCCATT IGCACACGGCAGG ACCTAACAGATGTC	A	T	Pro	SILENT-CODING	MHC	Human Gene Homologous to SPTRNL-ID:Q95368 HLA CLASS INHIBITOR Y NK RECEPTOR, HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
84	cg42686553	492	TGAGCATCTACCAT CTATCAGGGAAG AAGGGAAAGCCA TGAACTTAGGCTC	G	A	Glu	SILENT-CODING	MHC	Human Gene Homologous to SPTRNL-ID:Q95368 HLA CLASS INHIBITOR Y NK RECEPTOR, HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19

85	cg3337333	699	C T C T A G T A G T T G G T C C T T A C C C A C T A T G A A C C A A G T C A A A A C T G T A C G	T	A	Thr	SILENT-CODING	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HL-A CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
86	cg3337333	774	G G T A C T C A G T G G C C A T C A T C T C T / C T J A C C A T C T C T C C T T C T T C T C C T C	C	T	Phe	SILENT-CODING	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HL-A CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
87	cg3337333	783	T G G C C A V A C C C T T T C A C C A T C T C / C J C C T C T T G C T T C A T C G C T G T	T	C	Leu	SILENT-CODING	MHC	Human Gene Homologous to SPTREMML-ID:Q95368 HL-A CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
88	cg3394759	649	A G G A G T C A Q C G T G A G G G C C G A B A C T J C T A G G G A G C G G G A A G G G A G G A G T	C	T	Thr	SILENT-CODING	misc_channel	Human Gene SPTREMML-ID:Q14193 H-DRK1 K(+)-CHANNEL (HUMAN), 858 aa.	0	20
89	cg39660131	990	T C A T G G G C A A C T A A G G C A C A A T G I C T T G T C G C A A C T C A C A G C C T C A A C G	C	T	Cys	SILENT-CODING	misc_channel	Human Gene SPTREMBL-ID:Q14524 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 2016 aa.	0	3 (3p24)

90	cg44963814	717	CGGAATACCTGGC CATCAACTCTTAA[A] GAGCAGAAGAGAA CTGCACGGCGTC C	A	G	Glu	Glu	SILENT-CODING	misc_channel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa/pst; TREMBL NEW- ID:GI2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-13 19 (1q13.1)
91	cg21413267	870	AGAGTGCCGAGTC GCTCATCTGGAAAC /TGGCGTGGAC CTAACACACAAAG A	C	T	Asp	Asp	SILENT-CODING	misc_channel	Human Gene Similar to SPRENBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAenorhabditis ELEGANS, 461 aa.	7.90E-79
92	cg21413267	909	ACAACACAGGAA GTACGAGTCTGTC /TGGCGAGACTTA CCGGAGACATACC T	C	T	Cys	Cys	SILENT-CODING	misc_channel	Human Gene Similar to SPRENBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAenorhabditis ELEGANS, 461 aa.	7.90E-79
93	cg3000465	1160	AGAGGCTCTCTG CAGAACACTTC CIAATTACTTTG ATGAAAGATCATG	A	C	Pro	Pro	SILENT-CODING	misc_channel	Human Gene Similar to SPRENBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAenorhabditis ELEGANS, 461 aa.	6.10E-70 8 (8p11.2)

94	cg30421838	3766	GTCAGGATGGAG ATCCACAAACATC /TGTCAATGGCCA GATGCTTAATTG	C	T	His	His	SILENT- CODING	nucel_recept	Human Gene SWISSPROT- ID:PO6401 PROGESTERONE RECEPTOR (PR)-HOMO SAPIENS (HUMAN), 933 aa;length:SWISSPROT-ID:PO6401 PROGESTERONE RECEPTOR (PR - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (1q22)
95	cg30421838	4114	ATAACTTGATGA TCCTGAAACAA/ATC GCTTCATCTGATC TCCTGAAATCAT	A	G	Gln	Gln	SILENT- CODING	nucel_recept	Human Gene SWISSPROT- ID:PO6401 PROGESTERONE RECEPTOR (PR)-HOMO SAPIENS (HUMAN), 933 aa;length:SWISSPROT-ID:PO6401 PROGESTERONE RECEPTOR (PR - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (1q22)
96	cg43947341	713	TTCAGTCGCCAAA TTCCCCAGGGCACIA /GTTTGCGCAGCAA CTTCAGTACGGGA T	A	G	Asn	Asn	SILENT- CODING	nuclease	Human Gene Homologous to SWISSPROT-ID:PO7992 DNA EXCISION REPAIR PROTEIN ERCC-1 -HOMO SAPIENS (HUMAN), 297 aa.	1,10E+115	
97	cg43939210	4226	TCCCTGTACCCA GGCAAGTGATGIA /GTTGACACCTGTT CGTGACCTGGCCA G	A	G	Thr	Thr	SILENT- CODING	oncogene	Human Gene SYTREMBL- ID:099907 LATENT TRANSFORMING GROWTH FACTOR-BETA-BINDING PROTEIN-2 -HOMO SAPIENS (HUMAN), 1621 aa.	0	14 (1q24)

98	cg42674136	1447	CGGCCACACAGGCC GTCGCCGGAGC/C /TGTCGCCAACCC CAGGCCCTGGCCA	C	T	Ala	Ala	SILENT-CODING	oncogene	Human Gene SWISSPROT-ID:3134 HOMEBOX-PROTEIN HOX-11 (TCL-3 PROTO-ONCOGENE - HOMO SAPIENS (HUMAN), 330 aa.	3,70E-182	10
99	cg41972699	742	AGAACTCGGGGT CTCCCACTACATC/ TJATCAACTCGCTG CCCCAACCGCCGTT	C	T	Ile	Ile	SILENT-CODING	oncogene	Human Gene Similar to SWISSPROT-ID:064010 PROTO-ONCOGENE C-CRK (FAS) (ADAPTER MOLECULE CRK) - MUS MUSCULUS (MOUSE), 304 aa.	2,40E-84	22 (22q11)
100	cg42484556	963	CTGCAACTACCTTG AAACGATTAGIC/ TTGGGATCCACC CTCAGCAGAGCC	C	T	Leu	Leu	SILENT-CODING	oxidase	Human Gene SWISSPROT-ID:PI9878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) p67-PHOX - HOMO SAPIENS (HUMAN), 526 aa.	2,00E-287	1 (1q25)
101	cg43996195	1310	CAGCATGACCTGG CACTTACTCGG/A AIGGAAACTGG GATTCACTGTG	G	A	Pro	Pro	SILENT-CODING	phosphorylase	Human Gene SWISSPROT-ID:PO491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (NOSINE PHOSPHORYLASE) (NPY) - HOMO SAPIENS (HUMAN), 289 aa.	2,40E-155	

102	cg43996195	1421	TTCGAACCTGAGG TCGGTGCTAGT(G/ A)TAGAGACAGAG CCATTCTGCACTGT	G A	His His	SILENT-CODING	phosphorylase	Human Gene SWISSPROT- ID: P0491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (NP_000101) (HUMAN), 289 aa.	2.40E-155		
103	cg43948227	372	TTAACAGTTCTT ACTGCATCATCAT JATGTCAGAAATCT GTTCCCTTCAGCT	A	T	Ile	SILENT-CODING	polymerase	Human Gene Similar to SWISSNEW-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PCA) (P14) -HOMO SAPIENS (HUMAN), 126 aa/polymerase SWISSPROT- ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PCA) (P14) -HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5

104	cg43333426	1302	AGAGCCACTACAA GGTGGACTACIA .GCGTTTCAACAG ACCTACGAGGTGG	A	G	Ser	Ser	SILENT-CODING	potassium Chan nel	Human Gene SWISSPROT ID: P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INVARDLY RECTIFYING, SUBFAMILY I, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HHR) (HRK1) (HHRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa alias=SWISSPROTID:P48050	4.40E-241

105	cg33051431	1683	TCAACACTGTCCTGT ACCTGGAGGAAT CIGAGTCTACAGAA GTTGACTACACAA	T	C	Asp	SILENT-CODING	potassium Chan nel	Human Gene SWISSPROT- ID: P48051 G PROTEIN- ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 2 (GIRK2), (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY I, MEMBER 6) (KATP-2) (BIR1) (KIR3.2)- HOMO SAPIENS (HUMAN), 423 aa; ref/TREMBL NEW. IDG151826 INWARDLY RECTIFYING POTASSIUM CHANNEL KIR3.2-HOMO SAPIENS (HUMAN), 423 aa.	1.60E-227	16
106	cg3320929	1081	GGAGGATCACCTG CACCCCTTGCGC/ GIACCATGATC/C ATCCAGCTGCTA	C	G	Val	SILENT-CODING	proteaseinhib	Human Gene SWISSPROT- ID: P07093 GLIA DERIVED NEKIN PRECURSOR (GDN) (PROTEASE NEKIN) (PN-1) (PROTEASE INHIBITOR 7)- HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
107	cg33059041	624	AGICAGACACCGAG CTTAGAAATGAC/C TTATGGUCAATGC CTTGTTCCTGATG	C	T	Thr	SILENT-CODING	proteaseinhib	Human Gene Similar to SWISSPROT-ID: P17475 ALPHA- 1-ANTIPROTEINASE PRECURSOR (ALPHA-1- ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR)* RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83	14 (14q32.1)

108	cg01480266	1385	GGAGGACAGGCAA CTCATCCAGAAC /TTAGTCATACGCA AGATGAACAGCT	C	T	Leu	SILENT- CODING	Human Gene SPTRMBL- ID:Q92771 SYNAPSIN IB - HOMO SAPIENS (HUMAN), 478 aa.	2.90E-260	3 (3p)
109	cg42894986	1002	AACCGTCTCTGC CCACCCACTGAGC AIGCCCAAGGCGT GACTCTTGTTGG	G	A	Glu	SILENT- CODING	Human Gene SPTRMBL- ID:Q928686 50-KDA DISTROPHIN-ASSOCIATED GLYCOPROTEIN PRECURSOR - ORYCTOLAGUS Cuniculus (RABBIT), 387 aa.	1.40E-180	17
110	cg43961212	2160	TCTGGAAAGCCGGA CATCCCTCTGAGTA/ GIACTGACTGTATC CCTGGCGAACCA	A	G	Leu	SILENT- CODING	Human Gene Homologous to TREML NEW ID: G1703715 PANTOPHYNSIN-SYNAPTOPHY- SIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	7
111	cg42898003	497	TCTATGAGATTIC GATCTCTCTGTC/C AIGTCAGCTGTCC CCGGAGGCCCTGA	C	A	Thr	SILENT- CODING	Human Gene Similar to SWISSPROT-ID:P02585 TROPONIN C, SKELTAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
112	cg43960684	788	GCTTGGAGGAGGA GGGGGGTTGCGC/C /GIGACGACACTGA GGGGGCCATCCCG G	C	G	Arg	SILENT- CODING	Human Gene Similar to SWISSPROT-ID:P02535 KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (56 KD CYTOKERATIN 10) (56 KD TYPE I CYTOSKELETAL KERATIN, MUS MUSCULUS (MOUSE), 568 aa.	8.30E-58	8

113	cg43958714	1049	TTCGGAAAGGCCA AGCACTGACCCTG /C/TGATGATGC CACCAATATGCCA G	G	C	Leu	SILENT-CODING		Human Gene Similar to SQUALENE SYNTHASE (EC 2.5.1.21) (FARNESYL- DIPHOSPHATE FARNESYL TRANSFERASE) (FARNESYLTRANSFERASE) (PRISQUALENE-DI- DIPHOSPHATE SYNTHASE) - GLYCVRHIZA GLABRA, 412 aa.	9.20E-83	8
114	cg43124627	901	ACACCCACAGGAG TTTGGTTTA GGAA TTTATCTGTAAAT GGAAAGTTCTGC	A	T	Gly	SILENT-CODING		Human Gene Similar to SWISSNEW-IDP59062 ACETYL COENZYME A SYNTHETASE (EC 6.2.1.) (ACETATE-~COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa./dele/SWISSPROT-IDP59062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.) (ACETATE-~COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.70E-79	16

116	cg43064068	1484	TGTTGGTTCCTGGCC TCGAGTTCTCGA ITCCCATGACCA AACAGCTACCA	G	A	Leu	SILENT-CODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa db ss SWISSPROT-ID:P39062	7.40E-65	
117	cg43064068	1622	TCA CAG GAA AAT TCA ACG AGC CAAG /A/CTTCAGACAA GGAGTGGAAAGATG	G	A	Lys	SILENT-CODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa db ss SWISSPROT-ID:P39062	7.40E-65	

118	cg41084924	1278	TGACTCTCCGGAC CGTCCCAACAGTC GGTCTCAAGAGCA CTCCGAGACGCC	C	T	His	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:14416 D2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
119	cg41084924	1662	TCCG6AAAGGCCCT CCTGAGATTCCTC/ TCAGCTGCTACTC/ TGCTGCCGCGCG	C	T	Leu	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:14416 D2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
120	cg41084924	606	TCCCTGTCGCACAC CTGGCATGCGCTGA TTGGATGCTTACCG TGGAGGTGGTAG	C	A	Pro	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:14416 D2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
121	cg43985000	1471	TTCGCTCTTCGCTGG TTCCCTCTCA(C/T) TTAAGCCGTATT GAAGAAAATG	C	T	His	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
122	cg43985000	1597	TATGAAAGAAAC TGTGATACAGAA /GATGAGACAGAA CGATGTGAATTA C	A	G	Glu	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4

123	cg4930578	561	ACGTGAAACACCGA CATCTACTCCAA(G) AATGGCTGGTGACC GCGCTGTAACTCTGG	G	A	Lys	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P30989 NEUROTENSIN RECEPTOR TYPE 1 (NTR-R-1) (HIGH-AFFINITY LEVOCABASINE- SENSITIVE NEUROTENSIN RECEPTOR) (NTR1) - HOMO SAPIENS (HUMAN), 418 aa.	\$,00E-217	
124	cg3003519	1263	ATTCCCTGATGGCT JAAAAGGACCTTAAGT AGGACCCCTTAAGT ACATACCTACTG	C	T	Tyr	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P32247 BOMBESIN RECEPTOR SUBTYPE-3 (BRS-3) - HOMO SAPIENS (HUMAN), 399 aa [geht SWISSPROT- ID:P32247 BOMBESIN RECEPTOR SUBTYPE-3 (BRS-3) - HOMO SAPIENS (HUMAN), 399 aa [geht TREMBLNEW- ID:21240254 BOMBESIN RECEPTOR SUBTYPE-3 (UTERINE BOMBESIN RECEPTOR, BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.	3,00E-212	X

125	cg3003519	711	C T A G T G T G T A T C A T T C A G T G G G C T T A T C C T G G A A A T C C T A T T C T C A T C A	C	T	Gly	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:F32247 BOMBESIN- RECEPTOR SUBTYPE-3 (BRS-3) - HOMO SAPIENS (HUMAN), 398 aa/pols SWISSPROT- ID:F32247 BOMBESIN- RECEPTOR SUBTYPE-3 (BRS-3) - HOMO SAPIENS (HUMAN), 398 aa/pols TREHALYL NEW- ID:BE1240254 BOMBESIN RECEPTOR SUBTYPE-3 (UTERINE BOMBESIN RECEPTOR, BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.	3.00E-212	X
126	cg43969010	1182	T C G A A A G A G A T C T I G G A G G T G T A I C / T C A G G G A C T G T G C C A G A A A G G G G C	C	T	Tyr	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P0411 B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)* - HOMO SAPIENS (HUMAN), 391 aa.	9.00E-211	12 (14q32.1)
127	cg43263108	1097	A G A C A C C C / T T C C C A G C T G C G C T C / A I G G A G G A G G G A C C C A A G G G C C C T	C	A	Ser	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P43119 PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR)* - HOMO SAPIENS (HUMAN), 396 aa.	8.30E-208	19 (19q13.3)
128	cg43263108	272	G C C O C T G G G C T C G G G T G C T G T C / G I A C G G G A C T G C G G C C A C C G A C C T C	C	G	Val	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P43119 PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR)* - HOMO SAPIENS (HUMAN), 396 aa.	8.30E-208	19 (19q13.3)

129	cg43267238	1220	CCAGACTGGTCT GGTGTGGTGGTGCIA /GKTCCTCCTCGTC TGCTGGACTCCCA	A	G	Ala	SILENT- CODING	tm ⁷	Human Gene SWISSPROT- ID: P41145 KAPPA-TYPE OPIOID RECEPTOR (KOR-1) - HOMO SAPIENS (HUMAN), 380 aa.	2.10E-204	8 (8q11.2)
130	cg43267238	392	CAGGACATCAGCAT GGAATCCCGATC /TCAAGATCTCCGC GGGAGCGGGCC	C	T	Ile	SILENT- CODING	tm ⁷	Human Gene SWISSPROT- ID: P41145 KAPPA-TYPE OPIOID RECEPTOR (KOR-1) - HOMO SAPIENS (HUMAN), 380 aa.	2.10E-204	8 (8q11.2)
131	cg43267238	413	CGATCCAGATCTC CGCGGGGAGCGCG TGGCGCTACTCG GCCCGAGGCGCT	G	T	Phe	SILENT- CODING	tm ⁷	Human Gene SWISSPROT- ID: P41145 KAPPA-TYPE OPIOID RECEPTOR (KOR-1) - HOMO SAPIENS (HUMAN), 380 aa.	2.10E-204	8 (8q11.2)
132	cg43264978	155	TGGATCTGCACCTC TTGGACTACTCAIC /GAAGCCAGGGAAC TTCTCGGACATCA	A	C	Ser	SILENT- CODING	tm ⁷	Human Gene TREMBLENEW- ID: C2736282 G PROTEIN- COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
133	cg3001696	1154	C CGCGCACCGTG CATCGCGCTGGC /TTAACGCGCAATAG CAGCCCTAACCCC G	C	T	Gly	SILENT- CODING	tm ⁷	Human Gene SWISSPROT OI- ID: P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.10E-195	1 (1p36.1)

134	cg3001696	815	TGGCTGTGACCG TCCCCGGAGggg TGCGAGTGGTGTG CATGCTCCAGTTCC	G	T	Gly	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.10E-195 1 (1p36.1)
135	cg42704646	407	TGGCCTGCCGAIC ACCATGCTGCCTCA JACTGTTGCGGG GCAAACGACTGG	C	G	Leu	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (EP3 RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194 1 (1p31.2)
136	cg43326635	347	GGGATGCCACCT CTCCTCATGGTC GTTGGCTGGCGTG GCTGATGTGCCCG	C	G	Val	SILENT-CODING	tm7	Human Gene SWISSPROT- ID:P30542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173 1
137	cg303708	358	CCAACTCCCTCGT GGCTGCTGACAA GICAGATGATTC GTTTCATGTTG	A	G	Thr	SILENT-CODING	tm7	Human Gene TREMBLYNEW- ID:E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.50E-160
138	cg303708	787	GGTGGAAAGCCT CTCCACCTGGTT CTCTCACCTGGCT GTGTTCTCT	T	C	Gly	SILENT-CODING	tm7	Human Gene TREMBLYNEW- ID:E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.50E-160

139	cg3033708	841	ACAGCACCATCAT TGCTGTATTTC CIAACCCCTGTC TCCCCATCAGCTG	T	C	Phe	SILENT-CODING	tm7	Human Gene TREMBBLE NEW- ID:E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.30E-160
140	cg36729339	537	A�TCATCAAGTAC TTTTCTCTCTGCT AACCTCTCTCTT GGACCTCTGCT	C	T	Ser	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:Q15062 OLFACTORY RECEPTOR-LIKE PROTEIN FAT11 - HOMO SAPIENS (HUMAN), 316 aa.	1.90E-153
141	cg38841806	717	GACATCAGGGCA CGGTGCCAACCTC /GIGGCCATCTGCA GGCCAAAGAAAG T	C	G	Leu	SILENT-CODING	tm7	Human Gene Similar to SWISSPROT-ID:PF30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 9D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-57
142	cg38841806	723	AGGGGCAAGGGC CAACCTCCGCAAT CCTGAGGCAAG AAGAGTTTGTA	T	C	His	SILENT-CODING	tm7	Human Gene Similar to SWISSPROT-ID:PF30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 9D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-57
143	cg38841806	96	CAGGCTCTCATG CCCAGCTGGAG AICGGCACTGTGG GCACCAAGCTTAC	G	A	Gln	SILENT-CODING	tm7	Human Gene Similar to SWISSPROT-ID:PF30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 9D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-57

144	cg43040273	1966	CCCTGTCGTGATC TG GTCATGGGCTG/C AAGCACTGTGCC TTGGGGCCCC	G	A	Leu	SILENT-CODING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (53:2)
145	cg43040273	2237	CTGGCCATTAGA C TGCACTGACAC/G A/GGCCACCAAC AGGAAGCCATAA	C	A	Arg	SILENT-CODING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (53:2)
146	cg43336100	637	TGGAAACCGTGC A TCCAATGAGACCA T/TATGAGGCTGA GCTTTAGTGGCT	A	T	Pro	SILENT-CODING	tnf	Human Gene SWISSPROT- ID:P26022 PENTAXIN- RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (33:2)
147	cg21646034	376	GTTGGAGCAGAGA A TGCGAGAACAA/A /GTTGGACCAAC ACCATTACATA/TG G	A	G	Lys	SILENT-CODING	transcripfactor	Human Gene SWISSPROT- ID:Q00545 GABA B RING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR EATF1-4D) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	13

148	cg43916882	1608	TGGAGCTAACG CACACTCCGAA GCGCTCAATAAAG GCACTGATGCT	A	G	Gly	SILENT-CODING	transferase	Human Gene SWISSPROT- ID:P39656 DOI:CHY1- DIPHOSPHOOLIGOSACCHARI- DE-PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.19) OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT (DHOST 48 KD SUBUNIT) (KIAA0115) (HAA0643) - HOMO SAPIENS (HUMAN), 436 aa.	5.30E-245	1
149	cg2537639	294	TGGCTCCATTTC TGGAGGCCAC/ GTTCAACATCGAC ATCTCAAACAGC	A	G	Thr	SILENT-CODING	transferase	Human Gene SWISSPROT- ID:P16442 FUOSYGLYCOPROTEIN ALPHA-N- ACETYL GALACTOSAMINYL TRANSFERASE (EC:4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUOSYGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGA7)- HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (93%)

150	cg2537639	654	AACGTGACATGGAC CTTGTCCGGACAGC TGTTGGCGCTGGAA GATCCCTGACTCCG C	C	T	His	His	SILENT-CODING	transf erase	Human Gene SWISSPROT- ID:P16442 FUCOSYGLYCOPROTEIN ALPHA-N- ACETYLGLACOSAMINYLT RANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE / FUCOSYGLYCOPROTEIN 3- ALPHA- GLACOSYLYLTRANSF ERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSF ERASE) (B TRANSFERASE) (NAGAT)- HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9434)
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151	cg2537639	678	ACGTGGCTGGAA G GATCCTGACTCCQ/G AATGTTGGGCC CTTCACCCCCGCT	G	A	Pro	SILENT-CODING	transf erase	Human Gene SWISSPROT- ID:P16442 FUCOSYGLYCOPROTEIN ALPHA-N- ACETYLGALACTOSAMINYLT RANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGA) HOMO SAPIENS (HUMAN), 354 aa.	6-50E-192	9 (9434)
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152	cg2337639	768	GGCCCCAATGTTCCA GGCTTACATGCCCTCA TIAAGAACGAGGG CGATTCTACTACC	C	T	Pro	SILENT- CODING	transferease	Human Gene SWISSPROT- ID:P16442 FUCOSYLGlycoprotein ACETYL GALACTOSAMINYL TRANSFERASE (EC: 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE)/ FUCOSYLGlycoprotein 3, ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGA-T) HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)

153	cg2537639	927	ACGAGAGCCACT GAACAGTACCTTG /A/CTGCCGCCAA ACCCACCAAGCTG C	G	A	Leu	SILENT-CODING	transf erase	Human Gene SWISSPROT- ID:P16442 FUCOSYGLYCOPROTEIN ACETYL GALACTOSAMINYLT RANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT)- HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q44)
154	cg44000740	732	GGGGAGATACTGG CTAACCGAGAAIA /CJACAGGAAACAT CACCTTATCCAC A	A	C	Val	SILENT-CODING	transf erase	Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S- TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS:THETA)- HOMO SAPIENS (HUMAN), 239 aa.	1.50E-117	16

155	cg38859466	1183	ACGGAGTGGCGT GGGTCCTCTTCGTC/ TGGCTCTTCGCC AGTCTTCAGTGT	C	T	Cys	SILENT-CODING	transport	Human Gene SWISSPROT- ID: P3025 HIGH-AFFINITY CATIONIC AMINO ACID (CAT1) SYSTEM Y+ BASIC AMINO ACID TRANSPORTER (ECOTROPHIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPHIC RETROVIRUS RECEPTOR HOMOLOG) - HOMO SAPIENS (HUMAN), 629 aa.	0	13
156	cg40351913	1347	CCATGCCACGCT CCCTCTCTCTCA/ GAGCTGGCCGTC GTCCTCTCATCA	A	G	Ser	SILENT-CODING	transport	Human Gene SWISSPROT- ID: Q01959 SODIUM- DEPENDENT DOPAMINE TRANSPORTER (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (Sp15.3)
157	cg43964039	1719	GATGGAACAGTC CTGGGTTCTTG/ ATGACTTTGCTG GCTCCCTGCG	G	A	Asp	SILENT-CODING	transport	Human Gene SWISSPROT- ID: P1166 GLUCOSE TRANSPORTER TYPE I, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-239	1
158	cg43992017	1656	GCGGTGCTGGT GATGGGTGGCGC/ GJGGGGTGACGC TCACCCCTCCC	C	G	Pro	SILENT-CODING	transport	Human Gene SPTRMEL- ID: Q1728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN mRNA - HOMO SAPIENS (HUMAN), 455 aa.	4.40E-241	

159	cg4394629	1238	CCGCTGTAAATGCC TGTGACATAGCTC/ TACCAAGCAGGAG GTCCCTGTGTTTA	C	T	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT- ACQ1:Q031 PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE-TRNA LIASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0	3
160	cg43955093	2875	CATTGACTTAGGG CTGTGGGGCATC /GICGCCAGTGT CCCTCATAGAG G	C	G	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT- ACQ1:Q084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
161	cg43955093	3385	AGCGAGCCAAGAG AGATCTGTTGAAJC /TGCACTCTTTC AGAATAACAGATA	C	T	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT- ACQ1:Q084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
162	cg43035918	517	CGCTGGCATAGGA CATGGGGCTTG /TGCCTCCGAGA GCTGGGGCTA C	G	T	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT- AC2:Q42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
163	cg43974592	234	AAATAACAGGGA TTGAGAAATGCGT /AIGAGCAGGGAA AGACGAAAGGAA G	T	A	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene REMTR3BML- ACCEI:296438 SEQUENCE 28 FROM PATENT WO9727323 - UNIDENTIFIED, 1829 aa.	0	2 (2q34)

164	cg43956384	206	AAGGAGCCACACGC TGCCACCATGAACTG TAACTAGCAACCTG GAGCCCCAAGACC A	C	T	Asp	SILENT-CODING	UNCLASSIFI	Human Gene SWISSPROT- ACCP13866 SODIUM/GLUCOSE COTRANSPORTER I (NA(+)-GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 664 aa.	0	22 (22q13.1)
165	cg4025634	2757	TGAAAGTATCAA TCCAGAAGGAAT AGCTGGAAATTG CCCTCTGTTCATA G	A	G	Lys	SILENT-CODING	UNCLASSIFI	Human Gene SWISSPROT- ACCP06430 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
166	cg43940037	2472	GCTGGCGCACTGC TAGCCTAGAGGT /A/GCCAGAACCTC CTA/GCCCCCG C	T	A	Ala	SILENT-CODING	UNCLASSIFI	Human Gene SWISSPROT- ACCP141250 GLYCYL-TRNA SYNTHETASE (EC 6.1.1.14) (GLYCINE-TRNA LIGASE) (GLYTES) - Homo sapiens (Human), 685 aa.	0	7 (7p15)
167	cg4024279	481	AAA/ACGACTTAC TGCCTTCTGAA/A GIGAACTTGCCAT GAGAAAAGAATT	A	G	Glu	SILENT-CODING	UNCLASSIFI	Human Gene SWISSPROT- ACCP0271 ALPHA- FETOPROTEIN PRECURSOR (ALPHA-FETOGLOBULIN) (ALPHA-1-FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	

168	cg43926814	1122	CATGAGTTTGATC CCAGCTTCTCT TCGCCATTCTC	C T	Glu Glu	SILENT- CODING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACQ13573 NUCLEAR- PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR (NCOX-62)) - Homo sapiens (Human), 536 aa.	5.00E-289	14
169	cg40918088	1778	TGGAGCTGGAT TACTGTATGATA/ GJGCCTTAAGAGCT GCTGATGAGCTT	A G	Glu Glu	SILENT- CODING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACR251854 TRANSKETOLASE 2(EC.2.1.1.1) (TK_2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.80E-287	X (Sg28)
170	cg43966985	1242	TCAACACCTACGT CCACTTCCAAKIGG /TJAAGATGAAGGG CTTCCTCCCTCG	G T	Gly Gly	SILENT- CODING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACR2701019 ANGOTENSINOGEN PRECURSOR - Homo sapiens (Human), 485 aa.	3.90E-257	1 (1q2)
171	cg43924009	770	TGGCTTGACAAA TTGCTTGAAGACIA /TTCGATCCAGTAA GTGGACTCTTG	A T	Arg Arg	SILENT- CODING	UNCLASSIFI- ED	Human Gene SPTREMBL- ACO043411 HYPOTHETICAL 49.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 442 aa (fragment).	6.90E-239	
172	cg42913861	2186	C ¹ GGGCAACGCC CTCAACAGTAGTIC/ GICCGTAGTAGCCG GTGGGTGCTAAGA	C G	Gly Gly	SILENT- CODING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP090529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3.00E-227	2 (2q11)

173	cg42913861	2354	GCGGAGCTGGCAC CACCAAAAGGGT CTTCGGTGCGACTC TTCCCTGGTCCA	C	T	Arg	SILENT-CODING	UNCLASSIFIED D	Human Gene SWISSPROT- ACCP00529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B-CHAIN) - Homo sapiens (Human), 407 aa.	3.00E-227	2 (2cen)
174	cg43929685	236	CATAGAAGGCCAG GAATCAGGAGACI CTTGGGTCTGTC CTGGATTATACAC C	C	T	Gln	SILENT-CODING	UNCLASSIFIED D	Human Gene SWISSPROT- ACCP29080 (2'- S)OLIGOADENYLATE SYTHETASE IB (EC 2.7.7.-) (2'-OLIGO(A) SYNTHETASE IB) (2.5A SYNTHETASE IB) - Mus musculus (Mouse), 414 aa.	2.40E-225	12
175	cg43929685	268	GGAGTCAGGAGAC CTGGGTCTGTC TTGGATTATACAC CAGCTCTAGGG	C	T	Gln	SILENT-CODING	UNCLASSIFIED D	Human Gene SWISSPROT- ACCP29080 (2'- S)OLIGOADENYLATE SYTHETASE IB (EC 2.7.7.-) (2'-OLIGO(A) SYNTHETASE IB) (2.5A SYNTHETASE IB) - Mus musculus (Mouse), 414 aa.	2.40E-225	12
176	cg43918561	53	CCATGCCAACCCC CGACCCACACAG /C/CACAGGCCA GGGCTCCAGG G	G	C	Thr	SILENT-CODING	UNCLASSIFIED D	Human Gene SWISSPROT- ACCP04177 TYROSINE 3- MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Ratius norvegicus (Rat), 498 aa.	2.10E-224	11 (1p15.5)

177	cg42343176	1885	A/T/T/A/T/G/A/T/T/C C/T/G/A/G/A/G/T/H/A/ G/J/A/G/A/G/T/A/G/A/C/T G/A/G/A/A/T/C/C/T/T	A	G	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACCO14902 INDOLEAMINE 2,3-DIOXYGENASE (EC 1.13.11.42) (IDO) (INDOLEAMINE-PYRROLE 2,3-DIOXYGENASE) - Homo sapiens (Human), 403 aa.	3.90E-218	8 (Sp12)
178	cg43956382	1146	A/A/A/G/A/T/G/A/T CG/A/T/G/A/G/T/A/T/T/C /T/A/T/C/C/CAG/G/C/T CC/C/T/T/A/C/A/A/C	C	T	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACCO109816 TUMOR SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 390 aa.	4.90E-211	11
179	cg43944681	979	C/A/C/A/T/G/A/G/G T/T/G/T/G/C/G/G/C/T T/T/G/G/A/G/G/G/C/C G/C/G/T/G/G/G/A/G/T	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACCO15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT)(M) - Homo sapiens (Human), 392 aa.	1.30E-210	19 (19q13)
180	cg43984681	1074	T/C/T/G/T/A/C/A/G/A C/A/G/G/A/C/C/T/C/A/C /T/A/T/C/C/A/C/C/T/G G/A/A/A/T/G/G/C/C/T/G	C	T	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACCO15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT)(M) - Homo sapiens (Human), 392 aa.	1.30E-210	19 (19q13)

181	cg43950996	1762	CTGGCGGTGAGAC GTCAGAAGCTGCCA /GIGGGGAGGGGC TCCCTGCGCACAG C	A	G	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL- AC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.20E-204	1
182	cg44024506	988	ACCAAGCCTGCGT AGTCACAGCGCA GAGGACTGTCCT TGCCCTACCTCCATG C	G	A	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL- AC:Q36074 TYROSYLPROTEIN SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 377 aa.	1.90E-200	22
183	cg43980381	1114	CTACCGCCAACTA TGACTTTGCTCTCA GIAAGAACGCGAC CTCACCAAAGGA G	C	G	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISS-PROT- AC:Q003385 GILANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGS FORM A (HALGEF) - Mus musculus (Mouse), 852 aa.	5.60E-191	9

184	cg42650960	501	TCCCCCTGGAGAA CTTACCACTCCGAACT TTGACTGGATGGA CGAGGAAATACCGC C	C	T	Asn	Ser	UNCLASSIFIED	Human Gene SWISSPROT- AC:Q10981 GALACTOSIDE-2- L-FUCOSYLTRANSFERASE 2 (EC 2.4.1.69) (GDP-L- FUCOSE-BETA-1-D- GALACTOSIDE-2-ALPHA-L- FUCOSYLTRANSFERASE 2) (ALPHA(1,2)FT 2) (FUCOSYLTTRANSFERASE 2) (SECRETOR BLOOD GROUP ALPHA-2-FUCOSYLTRANSFERASE) (SECRETOR FACTOR (SE) (SE2) -Homo sapiens (Human), 343 aa.	2.00E-189
185	cg3239389	1497	ACATGCCAGGTGT GTTGGACGGCGTC/ TACCGACATCATC/ ATTGCCAAACACC	C	T	Val	Val	UNCLASSIFIED	Human Gene SWISSPROT- AC:P09471 GUANINE- NUCLEOTIDE-BINDING PROTEIN (G0), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.40E-188
186	cg3946951	615	CAGTGACGGCAGG GTCAAAGTCCTTG/ AAGGTAGCCCTGG TTAAGGTGTAGA	G	A	Ala	Ala	UNCLASSIFIED	Human Gene SWISSPROT- AC:P09467 FRUCTOSE-1,6- BISPHOSPHATASE (EC 3.1.3.11) (FRUCTOSE-1,6- BISPHOSPHATE-L- PHOSPHOTDROLASE) (FBPase) - Homo sapiens (Human), 337 aa.	3.50E-178

187	cg43248117	1054	AACAGGCCACTG TGAGAACCACT GICGTGTTCAAGTC TTGGGAATGGCA G	G	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-HOMOLOG (NADPH-REGULATED THYROID-HORMONE BINDING PROTEIN)-Homo sapiens (Human), 314 aa.	1.20E-161 (16p13.1 1)
188	cg46027049	482	CCACAAATGTTAGG AGGTTATTAACTC/ TJAATCCCTCAAGT AAACAATAACGCA	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACCP1245 ARYLAMINE N-ACETYL TRANSFERASE, POLYMORPHIC (EC 2.3.1.5) (PNAT) (NAT-2) (ARYLAMINE ACETYLASE)-Homo sapiens (Human), 290 aa.	5.40E-157 (8p23.1)
189	cg43982075	499	CTGCGCATCTTCAG CCCTCTGAAGCTT CTGTCCAGAGCAG AACTTCCTCG	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SPTRMB1-AC-QL579 THYROTROPH EMBRYONIC FACTOR - HOMO SAPIENS (HUMAN), 303 aa.	1.20E-154 22
190	cg43942977	350	GGCTTCCCAGT CGGGACAATTGG TTTACAGACTATGTC AAACTGGGAAATA	G	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC-Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148
191	cg43942977	701	GGCAAGCTGAAGAT CACCAATGCTGGG /CIAOTGTTCTGAT GAGGAGTGTGAGC	G	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC-Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148

192	cg43942977	773	GGAGGTGTTGTTG GTCCAATATCCCTG/ TAAAGGACAGCA GGTAGACTGACAG G	G	T	Leu	SILENT- CODING	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148	
193	cg43985220	753	TGACACTGCCAG AAAAGGAAGG TGTCCTTGTAA TGTCAAAA C	T	G	Gly	SILENT- CODING	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC:P2918 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.2.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM-SENSITIVE MYO- INOSITOL MONOPHOSPHATASE AI)- Homo sapiens (Human), 277 aa.	5.10E-145	8
194	cg43985220	837	TCTGGTGACTGA GTTGGCTCTC/C/ TGAACACAGA GACTGTAGAATG G	C	T	Ser	SILENT- CODING	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC:P2918 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.2.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM-SENSITIVE MYO- INOSITOL MONOPHOSPHATASE AI)- Homo sapiens (Human), 277 aa.	5.10E-145	8
195	cg43946394	321	TAGAGCCACACA GGCTCCAGGTGIA /GGCCATUTCGTC TCATCATCCAAAG	A	G	Ala	SILENT- CODING	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC:Z9692 ELONGATION FACTOR 1- DELTA (EF-1-DELTA)- Homo sapiens (Human), 281 aa.	2.80E-144	19

196	cg3119818	1329	CTGACAGGTACAG GCCTTCTAGTTCA TCAATTTCACCTGG GGCACTTACAATG	C	T	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT:ACC:P0915 CARBONIC ANHYDRASE 1 (EC 4.2.1.1) (CARBONATE DEHYDRATASE 1) - Homo sapiens (Human), 260 aa.	6.90E-141	8 (8q22)
197	cg3118279	735	AGAAAGTGAAAGGG GCTGTGTCGCACTT/ GIGGACCCGATCA AGTCGACACACTA	T	G	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT:ACC:Q0195 MAD PROTEIN (MAX DIMERIZER) - Homo sapiens (Human), 221 aa.	1.20E-111	2 (2p13)
198	cg43325007	866	TGGGTCAAGGAT GTAGGCCCTCTT/C/ CAGACCGAGCG GCTCAAGGCAAC A	T	C	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TRIMBLNEW:ACC:AD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
199	cg319524111	402	GCCAAATAGGAT AGGCGACTACAGI A/GTTCCGATACA GTGACACCTGGA GC	A	G	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TRIMBLNEW:ACC:BA13472 CD89 D8R - HOMO SAPIENS (HUMAN), 191 aa.	2.10E-100	19 (19q13.4)
200	cg32380516	629	ACGGGGAGGAGCT GCAGATGGAACCT /T/GTGAGGAGGTC TTCGGGACTCTG	C	T	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TRIMBLNEW:ACC:AB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa.	6.80E-95	19

201	cg43963913	871	AGAGGTCTGGGG CGCCGAGGCCA GAAAGGCCCGCAA AGGGCCTGGCTC CT	G	A	Arg	SILENT- CODING	UNCLASSIFI- ED	Human Gene Similar to SPTRMB1,-ACC-014803 BC1- X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5..10E-90	11
202	cg40262905	682	TAGTGAAGGCCT GAAATATACTTG TCGAGGGAAAT TGCGAAACTAC T	G	C	Leu	SILENT- CODING	UNCLASSIFI- ED	Human Gene Similar to SPTRMB1,-ACC-014803 BC1- X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 167 aa.	1..30E-89	
203	cg43918168	915	CCTCATCAAGC ATCCGGACTCA TCGGGGCTGCC GTGGCGCTGGGC C	T	C	Pro	SILENT- CODING	UNCLASSIFI- ED	Human Gene Similar to SPSSPROT-ACC-P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCTE LCA) Homo sapiens (Human), 248 aa.	3..80E-85	9 (12423)
204	cg43259701	136	CGACGAGGTGTA CGCGAGGGAGA CTTTGAGAAAGC CAGCGACAGCTC TT	C	T	Leu	SILENT- CODING	UNCLASSIFI- ED	Human Gene Similar to SPTRMB1,-ACC-000961 IPL (IPL) HOMO SAPIENS (HUMAN), 152 aa.	1..30E-77	11
205	cg1527767	162	TUUUCCACGTA CAATGTACAGTA GCAAGGAGCTGG GGAAGGTCTTC C	A	G	Arg	SILENT- CODING	UNCLASSIFI- ED	Human Gene Similar to SPTRMB1,-ACC-G36907 T- CELL RECEPTOR ALPHA- CHAIN IAP38 V(A)10.1-J(A)1- HOMO SAPIENS (HUMAN), 135 aa (fragment).	5..60E-68	

206	cg0568986	316	AGAAGAGAGGCTG TGAACTCCCAAC TTGTGTGACTCAT CGGGTGGAGGCT	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P06881 CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CGRP-D) (ALPHA-TYPE CGRP). Homo sapiens (Human), 128 aa.	5.10E-58 11 (1p15.2)
207	cg2250133	300	TCATCCCTGAGCTCT AAGAAGCTCTCT CCTCAGTAGCTCT GGCTCTATCTCT	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to REMTREMBL-ACC:D1002868 T-CELL RECEPTOR BETA-CHAIN V REGION - HOMO SAPIENS (HUMAN), 112 aa (fragment).	8.50E-56 7 (7q15)
208	cg2526759	317	CCTGGTTGCCACT GAGGAGGAGACAT CIGTAACCTCTAA TCAGTTATGAAG	T	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to REMTREMBL-ACC:D31509 T-CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54
209	cg41664708	249	AAGCTCTGCTGA TCACAAGCAC /GTTGGTGAGAG CGTGTCTAGAGC A	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1 ALPH) - Homo sapiens (Human), 114 aa.	2.00E-54 1
210	cg3300673	1571	AGGGAGGGGGGA GGTAGAGCATGGG GAGAGCACAGGGC CTCACAGGGACT ACT	G	gap			SILENT-NONCODING	AT Pease_associat ed	Human Gene SPTRMBL-ID:093650 VACUOLAR-TYPE H+-ATPASE 115 kDa SUBUNIT - HOMO SAPIENS (HUMAN), 831 aa.	0 17

211	cg4328434	2370	AGTCAAATCAGA GAGGATAAAAAA A ap/AIGACATTAT ATTATTCGCTC C	A	SILENT- NONCOD ING	ATPase_associat ed	Human Gene Homologous to SPTREMBL-ID:Q18783 C52E4.5 -CAENORHADITIS ELLEGANS, 590 aa.	4.00E-121	6	
212	cg43132502	196	TAAGCATGGGG GCACAGGGAGG A ACGTGGGAGATG CCACCTGGGTC AC	C	SILENT- NONCOD ING	ATPase_associat ed	Human Gene Similar to SPTREMBL-ID:Q1532 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11	
213	cg43931765	606	GGTCCCCTGGTTT ATCCAAAGTCGT JGAGGGAGGAGC CTGGATGCTCT	G	T	SILENT- NONCOD ING	cadherin	Human Gene SWISSPROT- ID:PI8084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
214	cg43931765	607	GTCCCTGGTTA TCGAAGTCGT JAGGGACGCCACCT GGCATGGCTCTG	G	T	SILENT- NONCOD ING	cadherin	Human Gene SWISSPROT- ID:PI8084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
215	cg43931765	615	CTTATGCCAGCT CGAGGGAGG G p AGCCCTGGATG GCTCTGGCTAG A	wp	G	SILENT- NONCOD ING	cadherin	Human Gene SWISSPROT- ID:PI8084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3

216	cg43931765	660	TAGCAGGCCGGTG ACATGCCCCGC ap[TACCCCTTCGT ACAGGCACTGTTG GC	gap	T	SILENT- NONCOD ING	cathelin	Human Gene SWISSPROT- ID: P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
217	cg43931765	665	GCCAGGTGACATG GCCAGGCCACTTGA ap[TJCCGTGAAAG CACTGTGGCTCT G	gap	T	SILENT- NONCOD ING	cathelin	Human Gene SWISSPROT- ID: P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
218	cg43931765	668	AGGTGACATGGCC AGGCACCTCTCTGA p[TGTACAGGCACT GTGGGCTCTGTC C	gap	T	SILENT- NONCOD ING	cathelin	Human Gene SWISSPROT- ID: P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
219	cg43931765	668	AGGTGACATGGCC AGGCACCTCTCTGA p[TGTACAGGCACT GTGGGCTCTGTC C	gap	T	SILENT- NONCOD ING	cathelin	Human Gene SWISSPROT- ID: P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
220	cg43931765	668	AGGTGACATGGCC AGGCACCTCTCTGA p[TGTACAGGCACT GTGGGCTCTGTC C	gap	T	SILENT- NONCOD ING	cathelin	Human Gene SWISSPROT- ID: P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3

221	cg45952088	4769	AATCCACATTCGG CATCAGGAAAGCCA /C1AAGTCCAGTG GCCATTAGGTGCC T	A	C	SILENT- NONCOD- ING	cadherin	Human Gene SPTRMB1- ID:Q15065 OB-CADHERIN-1- HOMO SAPIENS (HUMAN), 796 aa.	0	16
222	cg44010957	1406	TCCCTATGAGGCCG CAAAGGAGACAGC TTTCAGGAATGAGT TCCATGTTGAGA T	G	T	SILENT- NONCOD- ING	cadherin	Human Gene SWISSPROT- ID: P27071 LEUKOCYTE ADHESION GLYCOPROTEIN LEF-1 ALPHA CHAIN PRECURSOR (LEUKOCYTE FUNCTION ASSOCIATED MOLECULE 1, ALPHA CHAIN) (CD11a) (INTEGRIN ALPHAI- -HOMO SAPIENS (HUMAN), 1170 aa.	0	16 (16p11.2)
223	cg43956560	1463	CAGTGCACTCTGG AAGATTTCACCTV CIGACCAAACAGTTC CTTCAGGCTTCAT	T	C	SILENT- NONCOD- ING	cadherin	Human Gene SWISSPROT- ID: P41511 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90- MEL) (LEUKOCYTE- ENDOTHELIAL CELL ADHESION MOLECULE 1) (ICAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)

224	c943956560	1492	CAACAGITCCCTCA G GCTTCATTCTGATC CCCCATTATC CCTCAAACCCCA	A	SILENT- NONCOD ING	cadherin	Human Gene SWISSPROT- ID:P14151-L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR), (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90- MEL) (LEUKOCYTE ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L)-HOMO SAPENS (HUMAN), 372 aa.	1.00E-218	I (1q23)		
225	c943956560	2242	TGCCTCCCTCC CTGCCCGAACAG AATCTTATCACT TACCTAGATCTA	C	A	SILENT- NONCOD ING	cadherin	Human Gene SWISSPROT- ID:P14151-L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR), (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90- MEL) (LEUKOCYTE ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L)-HOMO SAPENS (HUMAN), 372 aa.	1.00E-218	I (1q23)	

226	gb 3264626	428	TGGCACAGTGAAT AAAGGTGATGGTIT AAGGAGAAAGCA AACTAGGAAAGAT C	T	A	SILENT- NONCOD ING	cathepsin	Human Gene SWISSPROT- ID:PA43235 CATHESPINK PRECURSOR (EC 3.4.22.38) (CATHESPIN O) (CATHESPIN X) (CATHESPIN O2) -HOMO SAPIENS (HUMAN), 329 aa.	4.10E-183	1
227	gb 3011543	1972	ACCGAACCCCTTC ACCGCTGGGCGC/ GCCCAAGTGACTT TAACAAACTCTG	C	G	SILENT- NONCOD ING	collagen	Human Gene SWISSPROT- ID:PT2658 COLLAGEN ALPH A(VII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
228	gb 3011543	2096	CATACCAGTCA CTGCAAAGGGG CGJAACGTTGGG TIGCCTATTCAAG A	C	G	SILENT- NONCOD ING	collagen	Human Gene SWISSPROT- ID:PT2658 COLLAGEN ALPH A(VII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
229	gb 3933757	2546	GAACCGATAGG CTCTGGAGGCCJA CTTGGTCAGCTGC TTGGAATCCAGCA	A	C	SILENT- NONCOD ING	complement	Human Gene SWISSPROT- ID:PT0643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0	5 (5p13)
230	gb 41533795	64	TGTGGTGTGAC CTTGGCCTCCACG/ GAGTCCTCCAGC CTCTCCGACAC	C	G	SILENT- NONCOD ING	complement	Human Gene Homologous to SWISSPROT-ID:PT2560 COMPLEMENT C8 GAMMA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 202 aa.	1.40E-104	9 (9p34.1)

231	cgt2542496	168	AGCCCTCTCACC C CGGATAGATCTCT TTCACCCCTGGCC GCCTTGGCCA	C	T	SILENT- NONCOD ING	csf	Human Gene SWISSPROT- ID:P440225 THROMBOPOEITIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C- MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) -HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189 3 (3q26.3)
232	cgt2542496	179	ACCGGATAATT C CCTCACCCCTGQC/ TJCGCCTTGCC CACCTACTCTGC	C	T	SILENT- NONCOD ING	csf	Human Gene SWISSPROT- ID:P440225 THROMBOPOEITIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C- MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) -HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189 3 (3q26.3)
233	cgt2533258	1356	GTGGCTGACATT C GCCCTGCTGAAC/T JGGGGACTGGAA TGTTGGAGGGAGC	C	T	SILENT- NONCOD ING	csf	Human Gene Homologous to SWISSPROT-ID:P09919 GRANULOCYTE COLONY- STIMULATING FACTOR PRECURSOR (G-CSF) -HOMO SAPIENS (HUMAN), 207 aa.	1.50E-107 17 (1q11.2)

234	cg2753430	657	ACGACTTGGGCC TCGGATCTTTgg p(GIAGTCAAAGTC CAGCTCTTCTGT	gap	G	SILENT- NONCOD- ING	csf	Human Gene Similar to SWISSNEW-ID:PN8700 INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOETIC COLONY-STIMULATING FACTOR) (HEMATOPOETIC GROWTH FACTOR) (E-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR (MGCF) - HOMO SAPENS (HUMAN), 152 aa) [PAGES:SWISSPROT-1DP8700 INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOETIC COLONY-STIMULATING FACTOR) (HEMATOPOETIC GROWTH FACTOR) (E-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR (MGCF) - HOMO SAPENS (HUMAN), 152 aa]	1.10E-77	5
235	cg44036323	225	TGGGGCTTAAG GGCAACCCGGCG [C]GACCTCTTC CCTAGTGCGGG	G	C	SILENT- NONCOD- ING	dehydrogenase	Human Gene SWISSPROT- ID:PP0367 GLUTAMATE DEHYDROGENASE 1 PRECURSOR (EC 1.4.1.3) (GDH) - HOMO SAPIENS (HUMAN), 558 aa	5.80E-303	10

236	cg43918671	766	GAGAGACCAATTAA CTTACATCATGGTC/ TGGTTTATAGACA TTGAAATCATATC	C	T	SILENT- NONCOD- ING	dehydrogenase	Human Gene SPTREMBL- ID:Q14131 DIHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.10E-272 7 (7q11)
237	cg43057018	1995	AGTTCAATATACT TTTCCTCCACLgap/ GTTTGCTGAAT GAAAATTCTG	gap	G	SILENT- NONCOD- ING	dehydrogenase	Human Gene SWISSPROT- ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa. http://swissprot.expasy.org/P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209 4 (4q22)
238	cg44005808	3691	ACAAGACAGAAAC TGAAGTGCATTCG gapCIAAAGGTGTC AGAGAGCGGCC GC	gap	C	SILENT- NONCOD- ING	dna_mn_bind	Human Gene SWISSPROT- ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA- B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa. http://swissprot.expasy.org/P19838 NUCLEAR FACTOR NF-KAPPA- B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA- BINDING FACTOR KBF1) (EBP- 1) - HOMO SAPIENS (HUMAN), 969 aa.	0

239	c644005808	630	TCTCCCTCCCCAG CGGCAAGCCAGCgap G/C/GCCGCCCTAGG AGGGAGACCCAC C	G	SILENT- NONCOD ING	dna_ma_bind	Human Gene SWISS-NEW- ID: P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING PROTEIN NF-KAPPA- (EBP-1) (CONTAINS: NUCLEAR FACTOR NF-KAPPA- B P50 SUBUNIT) - HOMO SAPIENS (HUMAN), 669 aa [ipicks] SWISS-PROT; ID: P19838 NUCLEAR FACTOR NF-KAPPA- B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) DNA- BINDING FACTOR KBF1 (EBP- 1) - HOMO SAPIENS (HUMAN), 969 aa.	0
240	c643956159	1244	TGGGGAGTCAGG GTCAACCCACATAAG gap/A/GCCATGCCACCA CGGGTGCTAGGCC GC	A	SILENT- NONCOD ING	dna_ma_bind	Human Gene SPTREMBL- ID: Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159 10
241	c643956159	1248	GAGTCAGGGTCA CCCACATACATAGA gap/T/GCA/CCAGGTT GCTATGGCTCT	T	SILENT- NONCOD ING	dna_ma_bind	Human Gene SPTREMBL- ID: Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159 10

242	cg43956159	1268	TACCACTGACCAAC GGCTGTCTATTCGCG A/C/T/C/T/AAGGAA CCTTTTACGCCCT	G	A	SILENT- NONCOD ING	dmr_ma_bind	Human Gene SP1REMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
243	cg43956159	1342	CCTGGAGGCAACT GGTAGGGTGCGA GUCAACGGCACTGC TTGGCTGGAAACA CG	G	C	SILENT- NONCOD ING	dmr_ma_bind	Human Gene SP1REMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
244	cg43956159	1364	CAGAACGGCATGC TTGGCTGGAAACCG p/ACGGCATCCCT CTTCACGGCGG C	gap	C	SILENT- NONCOD ING	dmr_ma_bind	Human Gene SP1REMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
245	cg43971258	471	CAGAGCTTACGCTCT GGCTCTTACGGCGC TIAACAAGTTCAAC TCCTTCGCTCTG	C	T	SILENT- NONCOD ING	dmr_ma_bind	Human Gene Similar to SWISSNEV-ID:Q02353 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR H1 H1R2) (HELIX- LOOP-HELIX PROTEIN IN HIEF-1) - HOMO SAPIENS (HUMAN), 119 aa, pols.SWISSPROT- ID:Q02353 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR H1H1R2) (HELIX-LOOP- HELIX PROTEIN HIEF-1)- HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60 (1p36.13)	1

246	c843971258	508	TGCCCTGGCTCCGT AGCACCAAGTT CIAAGTCCTCAGGAA GGGATTGGTGA	T	C	SILENT- NONCOD- ING	data_rna_bind_in hif	Human Gene Similar to 35 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR H, H (R21)) (HELIX- LOOP-HELIX PROTEIN HEIR-1) -HOMO SAPIENS (HUMAN), 119 aa. [polS]SWISSPROT- ID-C02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR H, H (R21)) (HELIX-LOOP- HELIX PROTEIN HEIR-1)- HOMO SAPIENS (HUMAN), 119 aa.	1,30E-60 (1p36.13)
247	c843982507	3373	GATAACCCTGGCTG GATCAAGCTTG [C]TGTACTTGACCG TTTTATTAATCT	gap	C	SILENT- NONCOD- ING	cpN	Human Gene SWISSPROT- ID-P98155 VERY LOW- DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) -HOMO SAPIENS (HUMAN), 873 aa.	0 9 (9p24)
248	c843982507	3739	CAAAAAAATTTAT AAACTAATTTC [p]GTTAGCTATGAA GATATCTTACCT	gap	G	SILENT- NONCOD- ING	cpN	Human Gene SWISSPROT- ID-P98155 VERY LOW- DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) -HOMO SAPIENS (HUMAN), 873 aa.	0 9 (9p24)
249	c843982507	514	CCCTCTTCTCCCC TTTCCTCCCTC/CAC JGCCCCACCTCT TCCCTCTTGG	A	C	SILENT- NONCOD- ING	cpN	Human Gene SWISSPROT- ID-P98155 VERY LOW- DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) -HOMO SAPIENS (HUMAN), 873 aa.	0 9 (9p24)

250	cg41554010	1371	CTGCCCTGCCACCT GTCCTGCTGCTGCTggat TICCAAAAGAGATTC TGGTATGAACCTG	gap	T	SILENT- NONCOD- ING	eph	Human Gene SWISSNEW- ID:P06727 APOLIPOPROTEIN A- IV PRECURSOR (APO-AIV)- HOMO SAPIENS (HUMAN), 396 aa. [swissprot:ID:P06727] APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)- HOMO SAPIENS (HUMAN), 396 aa.	1:30E-203 (1:q23)	11
251	cg41554010	1371	CTGCCCTGCCACCT GTCCTGCTGCTGCTggat TICCAAAAGAGATTC TGGTATGAACCTG	gap	T	SILENT- NONCOD- ING	eph	Human Gene SWISSNEW- ID:P06727 APOLIPOPROTEIN A- IV PRECURSOR (APO-AIV)- HOMO SAPIENS (HUMAN), 396 aa. [swissprot:ID:P06727] APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)- HOMO SAPIENS (HUMAN), 396 aa.	1:30E-203 (1:q23)	11
252	cg43984905	2376	TCCCCTCAGACT AGGCTGAGGAAI GJCJCACTGGGT CCCCCTGAGTGG GC	G	C	SILENT- NONCOD- ING	esterase esterase	Human Gene SWISSPROT- ID:PF1178 1* PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODESTERASE DELTA 1 (EC 3.1.4.1) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-II) - HOMO SAPIENS (HUMAN), 756 aa.	0	3

253	cg43984905	2440	CACATGGGGGAC AGGCCTGGTGG /C/C/TGCTCAAGCC TC/TGCTCAGAGC	G	C	SILENT- NONCOD- ING	esterase	Human Gene SWISSPROT- ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.1) (PLC DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
254	cg43992911	382	CTAAAGTCGGAGT ATCTCTTCAGT/ A/JATTTCACGTCT GGCGCGCTTCA	G	A	SILENT- NONCOD- ING	glycoprotein	Human Gene SWISSPROT- ID:PO183 MULTIDRUG RESISTANCE PROTEIN 1 (P- GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0	7
255	cg43932434	267	TTCTCTAGGGGG TCTGTGAAGATG/ ATCTAACTACTAC ACCCCAACCCCCA	G	A	SILENT- NONCOD- ING	glycoprotein	Human Gene SWISSPROT- ID:PI6070 CD44 ANTIGEN PRECURSOR (CHILOGYCTIC GLYCOPROTEIN 1) (PGP-1) (HUTCH-1) (EXTRACELLULAR MATRIX RECEPTOR-II) (ECM-R-II) (GP50) LYMPHOCYTE HOMING/ADEPTION RECEPTOR (HEPARAN ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HSPG) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.8E-195	11 (11p1)

256	cgt33234	306	CCCCAACCCAA CCTCAATGTTGAAATA /GICAATGCCAGG GATTAGGTATGG A	G	SILENT- NONCOD- ING	glycoprotein	Human Gene SWISSPROT- ID: P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECM-R-III) (GP90)	1.80E-195 II (11pter)	
257	cgt3318219	366	GCGAGGTCTAGAG GGCGGCCGAGC A/GGCCCTCGCG AGGTCCCCAGGCC GG	A	G	SILENT- NONCOD- ING	glycoprotein	Human Gene SWISSPROT- ID: P13813 T-CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1)- HOMO SAPIENS (HUMAN), 335 aa [pkeys:SWISSPROT-ID:P13813] T-CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1)- HOMO SAPIENS (HUMAN), 335 aa	3.10E-185 I (1q21)

258	cg43967861	1954	CTC/TAT/ACT/GTACA/T CTC/ACCCATTAA/T/g gg/TCAAACACATAA GACCATGGTATAA A	T gap	SILENT- NONCOD ING	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q068378 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM- 90)-MUS MUSCULUS (MOUSE), 685 aa.	8.20E-67	2
259	cg43967861	1955	TCTATACTGTACAC TCACCCATAATT/g gg/CAAACATAC ACCATGGTATAA G	T gap	SILENT- NONCOD ING	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q068378 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM- 90)-MUS MUSCULUS (MOUSE), 685 aa.	8.20E-67	2
260	cg43965366	1411	GCGGAATAGCTG GGTTGGAAAAGC /TAATTTTGAAA TATOTGGATCT	C T	SILENT- NONCOD ING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALIUDIN)-MUS MUSCULUS (MOUSE), 690 aa.	8.90E-61	6 (6p25)
261	cg43965366	385	TACT/GAC/TTAAAT CACACCTAGACIA /TTATCGAGGGA AATTGACACATA A	A T	SILENT- NONCOD ING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALIUDIN)-MUS MUSCULUS (MOUSE), 690 aa.	8.90E-61	6 (6p25)

262	cg43322513	1255	TGTCCTTGAAAGAA CATGCACCTGGCCTGCA /GICGGATGCA A A	G		SILENT- NONCOD ING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL- RICH HYDROXYPROLINE- RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	I2	
263	cg41637704	1397	CCCGGGCCAGT AGGAGCCCCCG /p/GJCCCAAGAGGT GGGGGGCGCACGG AG	gap	G		SILENT- NONCOD ING	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEOBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7
264	cg41637704	1423	CCAGCAGGTGG CGGGACGGAGG /p/GJCCCAAGAGGT GGGGGGCGCACGG AG	gap	G		SILENT- NONCOD ING	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEOBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7
265	cg41637704	1817	TGAAACTTGAAAC CGCCUCUUGGAGC /TGCCATITCTGAG AGTTTTGAAAA	C	T	SILENT- NONCOD ING	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEOBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7	
266	cg43980506	939	TCCAAGAAAGGGT CATCGAAGCTTAT /CTGGGAATAATC CTCTCAATTAGAA A	T	C	SILENT- NONCOD ING	homeobox	Human Gene TREMBLNEW- ID:Q2896172 LIM HOMEOBOX PROTEIN COFACTOR - HOMO SAPIENS (HUMAN), 373 aa.	1.60E-206		

267	cg43961305	100	G G G G G T T T T T T T T T T T T C T C G (G) T	G	T	SILENT- NONCOD- ING	Hydrolyase	Human Gene SWISSPROT- PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE)- BOS TAURUS (BOVINE), 289 aa.	1,30E-156	10
268	cg43998672	503	C T G G G G T T T C G G G G A G G A A C C A A G / G / G / A C C T C T G C T G C A	G	gap	SILENT- NONCOD- ING	Hydroxysteroid	Human Gene SWISSPROT- ID:Q13194 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2,00E-220	16 (1642)
269	cg43998672	505	G G G G G T T T C G G G A G G A C C A A G G G / G / G / C C T C T G T G C G C A G T	G	gap	SILENT- NONCOD- ING	Hydroxysteroid	Human Gene SWISSPROT- ID:Q13194 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2,00E-220	16 (1642)
270	cg42908571	1031	G A G T T A A T T A T G T A A G T C A T A T T I (gap/ T J A T A T T I T T A A G A A G T A C C A C T G A A	T	gap	SILENT- NONCOD- ING	interleukin	Human Gene Homologous to SWISSPROT-ID:Q05231 INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA(-2)) (HYBRIDOMA GROWTH FACTOR)- HOMO SAPIENS (HUMAN), 212 aa.	3,40E-108	7 (7p21)

271	cg42908571	1178	CTTACCTCAAATA AATGGCTAACTTGA ATTATACATATTIT TAAAGAAAATATT A	GaaP	T	SILENT- NONCOD ING	Interleukin	Human Gene Homologous to INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2 (BSF-2), (INTERFERON BETA-2), (HYBRIDOMA GROWTH FACTOR)-HOMO SAPiens (HUMAN), 212 aa.	3.40E-108	7 (7p21)
272	cg42164914	1617	CAGCCCCATTTGT GTCACAGAAGT /CAGAGGAGGCCA CGTCTTACTAGTT	T	C	SILENT- NONCOD ING	Interleukinreceptor	Human Gene SWISSPROT- ID:PF5202 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPiens (HUMAN), 360 aa.	9.60E-191	2 (2q35)
273	cg43958501	1133	CCCAACCTGGGTTT GGCGACATCA/A/ GAAATGATGAGTA CATTTGAGATA	A	G	SILENT- NONCOD ING	Isomerase	Human Gene SWISSPROT- ID:PF4926 PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6- PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0000)- HOMO SAPiens (HUMAN), 289 aa.	1.60E-156	\$

274	cg43958501	805	CACCCCCAGGTCT CCTAGTTTCAAGA[G/ A]AAAAAGCTGTA AAGTGGAAAGGG A	G	A	SILENT- NONCOD ING	Isomerase	Human Gene SWISSPROT- ID:Q4926 PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6- PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0600)- HOMO SAPIENS (HUMAN), 289 aa.	1.60E-156	5
275	cg43096950	2710	TATATCATTCCT ATCTGTGATGATG GTAAAAAGGGGG GGGCCAGCCCTG	T	G	SILENT- NONCOD ING	kinase	Human Gene SWISSPROT- ID:Q4739 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPYC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0	10
276	cg42879455	2239	AGCCCTTGCTCC CACTCAATACTAA CTAAAGGCCCTCT CTACATCTGGAA	A	C	SILENT- NONCOD ING	kinase	Human Gene SWISSPROT- ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.12) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 639 aa.	0	X (Xg21.3)

277	cg42879455	2283	AAAAAGGCCCTC TCTAACATCTGGG/A GATGGCACCTCTTC TTTGATTCCTGG	A	G	SILENT- NONCOD ING	kinase	Human Gene SWISSPROT- ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA) TYROSINE KINASE (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0	X (Xq21.3)
278	cg43971741	2151	AGCAACTTGCTG AGCCCCACACAA/C /TACAGAGAAATC ATCAACCTGACTT A	C	T	SILENT- NONCOD ING	kinase	Human Gene SWTPREMBL- ID:Q9Z749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN)* HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
279	cg43971741	2200	TAAGAGTTCAA GATGTCAACTTC AAGGCTGATCA/GC AGATGGGATGTGA	C	A	SILENT- NONCOD ING	kinase	Human Gene SWTPREMBL- ID:Q9Z749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN)* HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
280	cg43971741	2151	TTTTAAAAATCGA TCACACACATGgg /TGGTAATTAAG TATAAATTCTTTC	ggp	T	SILENT- NONCOD ING	kinase	Human Gene SWTPREMBL- ID:Q9Z749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN)* HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9

281	cg43947749	1996	AACGTGATTCGG ACCGTCAACCTG /gap GCCCGGCC TCCTACAGCTTA AC	G	gap	SILENT- NONCOD ING	kinase	Human Gene SWISSPROT- ID:149840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA)- HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
282	cg43947749	1997	ACGGTGAATCGCA CGCTCAACCTGIG /gap CCCTCCCTC CTACAGCTGAA T	G	gap	SILENT- NONCOD ING	kinase	Human Gene SWISSPROT- ID:249840 GL YCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA)- HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
283	cg4131752	1535	CACITAATACCGAG AGACACCCCCCG /gap CTTCCTCCCT CTTCCTCCCT	C	gap	SILENT- NONCOD ING	kinase	Human Gene SPTRMBL- ID:Q1599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA- 1)-HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
284	cg43917718	306	AGACGTGTCGCC ACAGGTCAGQA /GTTAACAGATGCC CTGTCCTACTGAGA G	A	G	SILENT- NONCOD ING	kinase	Human Gene Similar to SPTRMBL-ID:Q1599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA- 1)-HOMO SAPIENS (HUMAN), 450 aa.	1.40E-79	17
285	cg43928048	1876	TTGATGAAAGG TGGCCACACTGIG AGATTTATACAC ACTTGATGGAA	G	A	SILENT- NONCOD ING	kinase	Human Gene Similar to SWISSPROT-ID: P050530 KD PROTEIN KINASE HOMOLOG (EC 2.7.1.-) (PROTEIN B1)- VACCinia VIRUS (STRAIN COPENHAGEN), 300 aa.	5.30E-55	

286	cgt2714751	208	CCCTCCGGATTCG GC GGCGGTGGC /M/C/G/C/G/GAGT GAGGGTTTCGTG G	C	M	SILENT- NONCOD- ING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4) (P16- INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	2.60E-53	9 (9p21)
287	cgt3322545	2943	TCCAAGCTTGC CTGCCACTGGGIA (G)AAACTCCACCT CCCACTTCCAC	A	G	SILENT- NONCOD- ING	kinaseceptor	Human Gene SWISSPROT- ID:P34630 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. SwissProt:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)

288	cgt3322545	3037	CCACCTCCA'TGCCA GACAGTCCTC[C] GJCCTCTCTTG CAAGTACATACC	C	G	SILENT- NONCOD ING	Kinase receptor precursor (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa/pes/WS2P07-1D:P03050 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	Human Gene SWISSPROT- ID:P03050 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa/pes/WS2P07-1D:P03050 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
289	cgt3322545	3038	CACCTGATGCCA GACAGTCCTC[C] /GJCCTCTCTTG AGTAGCATACCT	C	G	SILENT- NONCOD ING	Kinase receptor precursor (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa/pes/WS2P07-1D:P03050 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	Human Gene SWISSPROT- ID:P03050 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa/pes/WS2P07-1D:P03050 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.12) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
290	cgt33980494	1040	GTC[GATAGAGA GGAGGAGGAA[A[GCAATCTGTTA AAACCTAGGAAT TC	A	G	SILENT- NONCOD ING	Kinesin	Human Gene SPTRMEL- ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN)- HOMO SAPIENS (HUMAN), 665 aa.	0	16

291	cg45925424	374	TCAAGGAGAAGGC /C/CATGTCCAAAT GGTGTACATAAAG	A	C	SILENT- NONCOD ING	kinatin	ID:007866 KINFESTIN LIGHT CHAIN (KLc) - HOMO SAPIENS (HUMAN), 569 aa.	1.90E-304	14
292	cg42479188	305	TTCGAAGAGGCT GACGATTACTA GTTCTACAGAA	A	G	SILENT- NONCOD ING	MHC	Human Gene Homologous to SWISSPROT-ID:P13765 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, D0 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 273 aa.	3.40E-147	6 (6p21.3)
293	cg42686558	1167	CTAGCTCCCTCC CATTCACAGAA CIACACATCTT GCTCTACCAAAAG	A	C	SILENT- NONCOD ING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, D2 ALPHA CHAIN PRECURSOR (MHC DIN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
294	cg33337333	1122	TGCTCAAACCCA GCTGCCAGCTCTV CHAATGTCACAGGA GCTGAAATCTGAA	T	C	SILENT- NONCOD ING	MHC	Human Gene Homologous to SWISSPROT-ID:Q95568 H.A. CLASS LINHIBITOR Y NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
295	cg27803682	2506	GTGGCTGGGTAT TCATCCATGCTTV GIAAGCACTTGA GCCTCGAGGTC	T	G	SILENT- NONCOD ING	misc _channel	Human Gene Similar to SPTREMBL-ID:P91197 SIMILAR TO JIGAND-GATEL IONIC CHANNEL PROTEIN- CABNRHABDITIS ELEGANS, 461 aa.	3.50E-81	

296	cg21413267	1440	CGAGGGGACCCA GAGCTGACCCCT /QICCTCACCTCC TTCGTGCTCCCC	T	G	SILENT- NONCOD- ING	misc_channel	Human Gene Similar to SPTRMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CATIONHABDITIS ELEGANS, 461 aa.	7.90E-79	
297	cg21413267	1860	AGGAGCCCTCTC GOTGTCCCCAGT /CIGCAACGGTCAA GACCGCACACC A	T	C	SILENT- NONCOD- ING	misc_channel	Human Gene Similar to SPTRMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CATIONHABDITIS ELEGANS, 461 aa.	7.90E-79	
298	cg21413267	1890	CGGTCAAGACCCG CAGCACCAAGCT AAGCGGCCGC ACTCCCTCTCG C	A	G	SILENT- NONCOD- ING	misc_channel	Human Gene Similar to SPTRMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CATIONHABDITIS ELEGANS, 461 aa.	7.90E-79	
299	cg42481172	1541	GAGGGCTGGGT GTGGCTCGGGA /CIGGGGTGAGC GCGTGCTCTATC	A	C	SILENT- NONCOD- ING	misc_channel	Human Gene Similar to SPTRMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CATIONHABDITIS ELEGANS, 461 aa.	2.30E-71	1
300	cg32518465	89	GGGGCAGGGCG GCCCTGGCAGG upCGTAGGCGATG AGCTTGCGCCA AT	gap	C	SILENT- NONCOD- ING	oxygenate	Human Gene SWISSPROT- ID:15198 VA1 PROTO- ONCOGENE • HOMO SAPIENS (HUMAN), 846 aa.	0	

301	cg4197699	627	ATGGGGGCCGCGGT CTGCCCAAGAGGAG sp/C/GAGAACCCGG CTCAGGGCAGC GC	Gpp	C	SILENT- NONCOD ING	oncogene	Human Gene Similar to 1010 PROTO- ONCOGENE C-CRK (378) (ADAPTER MOLECULE CRK)- MUS MUSCULUS (MOUSE), 304 aa.	2.40E-84 (22q11)
302	cg40333812	235	AGCATTTGAGGAA GCATAACTGAGC /TGGAAAGGGGT GTGGGGTACTTGC C	C	T	SILENT- NONCOD ING	oncogene	Human Gene Similar to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3)-MUS MUSCULUS (MOUSE), 1964 aa.	1.40E-62
303	cg43280482	2295	AGCATCTGAGAC GACCCCGCAGC /CTTCCTCTGGAC CCCCCTGAAGCC	A	C	SILENT- NONCOD ING	oncogene	Human Gene Similar to TRIMBLINEW-ID:G2952331 ARQ/ABL-INTERACTING PROTEIN ARKB2A-HOMO SAPIENS (HUMAN), 666 aa.	3.90E-62
304	cg4014837	22	CACTGCTGTGCGAG GGCAAGGAAATTGC TCCAGGGAGACAG CCCAAGCAAAG	A	T	SILENT- NONCOD ING	oxidase	Human Gene SWISSPROT- ID:PR0684 CYTOCHROME P450 3A4 (EC 1.14.14.1) (CYPIIA4) (NEDIPINE OXIDASE) (NF-25) (H44-PGN1)-HOMO SAPIENS (HUMAN), 502 aa.[pmols/WISSPROT-ID:PR0684 CYTOCHROME P450 3A4 (EC 1.14.14.1) (NEDIPINE OXIDASE) (NF-25) (P450-PGN1) -HOMO SAPIENS (HUMAN), 502 aa.	8.00E-237

305	cg41626506	3178	CAGCACAGGAGC GCTCTTATCTG/A gg CCCTTTTCCCT TTCAGCAACT	A	Ppp	SILENT- NONCOD ING	peroxidase	Human Gene SWISSPROT- ID: P07702 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TP0) - HOMO SAPIENS (HUMAN), 533 aa.	0	3 (3q26.3)
306	cg43918944	2958	TCTGTAGAGCTCTG AAAAGGTGAACTV GATATAGGGCT TGATGTTTAC	T	G	SILENT- NONCOD ING	phosphatase	Human Gene SPTRMBL- ID: Q1572 PROTEIN PHOSPHATASE 2A B5-ALPHA -HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
307	cg43988365	1537	GACAGACGAGACA GTGAGGTATGIGA /GGGGTGTGTCGG AATGGTCCGGAG C	A	G	SILENT- NONCOD ING	phosphatase	Human Gene SWISSPROT- ID: Q14642 TYPE I INOSITOL- 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE (EC 3.1.3.56) (SPTASE) - HOMO SAPIENS (HUMAN), 412 aa;alias: SPTRMBL-ID: Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5-PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.60E-227	10
308	cg43969460	581	TAATCTATGCAAGA CAAGCTTGTC /GTCACGTGGCGT CTCTAGTTGATT	C	G	SILENT- NONCOD ING	phosphatase	Human Gene SWISSPROT- ID: P156876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PP2A_B PHOSPHATASE PP2A_B SUBUNIT ALPHA (ISOFORM (ALPHA-PR55) - RAT/TUS NORVEGICUS (RAT), 447 aa.	1.90E-202	

309	cg43933809	362	AATTAACACCTA GGTGTATACTTAT CATTGAACTAGTT TATTTCCTATTAA	T	C	SILENT- NONCOD- ING	phosphatase	Human Gene SWISSPROT- ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PPI- BETA CATALYTIC SUBUNIT (EC 3.1.16) (PP1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.60E-181 2 (2p23)	
310	cg43931144	215	TGCTCGGGCGCTG CCACTAAGGTCATC /TTCGCCCTCCCGA GAGGCCAGAGCGG	C	T	SILENT- NONCOD- ING	phosphataseinhibitor b	Human Gene Similar to SWISSPROT-ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR 1PP2A (H1-A-DR ASSOCIATED PROTEIN) (PP1) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.20E-89 9	
311	cg42937321	1977	CTTTCCTCTTAC CCTCTCTCTG/T AACATCTAAACA ACAGACTTACG	G	T	SILENT- NONCOD- ING	potassium Chan- nel	Human Gene SWISSPROT- ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (KPCN3) (HKC3) (HUK3) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284 1 (1p21)	

312	cg42937321	1983	CCCTCTACCCCTC TCTCTGAACTCT GTAAACCAAACAGA CTTACGTAAACT	C	T	SILENT- NONCOD- ING	potassium Chan- nel	Human Gene SWISSPROT- ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL (Kv3.1) (HPCN3) (HGVS) (HUK3) (HLE3), HOMO SAPIENS (HUMAN), 523 aa.	5,40E-284	1 (1p21)
313	cg40991963	1357	CAAAATGTAACAG TGGCTTTCAAC/A GIGGAAATAAGCA AAGTCCTAAAGC T	A	G	SILENT- NONCOD- ING	potassium Chan- nel	Human Gene SWISSPROT- ID:P45048 ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 1 (KIR1.1) (HPCN1) (HGVS) (HUK1) (HLE1), SUBFAMILY 1, MEMBER 1 (ATP-SIGUALYED) POTASSIUM CHANNEL ROM- K1 (KIR1.1) • HOMO SAPIENS (HUMAN), 391 aa.	1,80E-205	11 (11q42)

314	283951366	2332	AAGAGATTTGAA TACTTAAACATGG AATCAAAAGATGC AAAATGCTGAAGG	G	A	SILENT- NONCOD- ING	prostaglandin	Human Gene SWISSPROT ID:PP3534 (PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1)) (CYCLOOXYGENASE-2) (COX-2) (PROSTAGLANDIN- ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PFS 1D)-1(HMO SAPENS (HUMAN), 604 aa. Ile¹Ser²Leu³Ile⁴Asp⁵Leu⁶Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN- ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE)-1 (HOMO SAPIENS (HUMAN), 604 aa.)	0	1 (1q:2.5:2)
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315	cg43951366	2829	TGGTGGAGCCACT GCAGTTGTTATCCTT CIAAAATAAGAAAT ATTTCGTGAGATA	T	C	SILENT- NONCOD- ING	prostaglandin	Human Gene SWISSPROT- ID:P3534 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) CYCLOOXYGENASE-2) (COX- 2) (PROSTAGLANDIN-L- ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PGS II) • HOMO SAPIENS (HUMAN), 604 aa/pes SPTRMEL-ID:Q16876	0	1 (q35.2)
316	cg43306254	1431	CACTTAACTGCACT GTGGCACGCTTC TTGTTAACAAATA CGCTAAACCTTA	T	C	SILENT- NONCOD- ING	prostaglandin	Human Gene SPTRMBL- ID:Q00325 PROSTAGLANDIN E3 RECEPTOR SUBTYPE ISOFORM • HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (p31.2)

317	cg43306244	1666	A/T/G/C/T/A/T/T/A/T/T/A/T/G/T/G/A/A/C/A/T/T/T/T/A/A/A/T/G/A/T/C/T/G/T/C/T/T	T	SILENT- NONCOD- ING	prostaglandin	Human Gene SYTREMBL- ID:Q00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211 1 (1p31.2)	
318	cg42918089	1064	C/A/T/C/G/A/A/T/G/A T/A/G/C/A/G/T/C/T/C/ T/T/C/C/T/C/T/C/T A/G/C/A/T/T/G/T/C/A	C	T	SILENT- NONCOD- ING	protease	Human Gene Homologous to SWISSPROT ID:P02237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PLMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN)- HOMO SAPIENS (HUMAN), 267 aa SwissProt:SWISSPROT-ID:P0237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PLMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN)- HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146 11 (11q2.1)
319	cg4032168	1703	T/C/C/A/T/C/C/C/T/T/T G/G/G/C/T/C/T/G/G/C J/A/G/G/A/G/T/A/C/A T/T/A/C/T/G/A/G/C/C	G	C	SILENT- NONCOD- ING	protease	Human Gene Similar to SWISSPROT ID:P2155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.40E-82 2 (7q13)

320	cg43154190	1250	TACCGGGAAAGTGT AAGCTCAATTGCAAT/ CCTCTGTGTTCTGG CCACAACTCCA	T	C	SILENT- NONCOD- ING	protease	Human Gene Similar to SWISSPROT-ID:50280 MATRIXLYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) • RATTUS NORVEGicus (RAT), 267 aa.	2.40E-59	11 (11q22)
321	cg43927549	175	CCCCATCTGGGG CTCTACTGGGG /CGTCGCGTC GAAAGATTCG A	A	C	SILENT- NONCOD- ING	reductase	Human Gene Homologous to SWISSPROT-ID:16033 NAD(P) DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) • HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
322	cg43927549	191	TACTGGGGAGTC GCTGGTCGAAAG aa/GIAATGCGGGAC TOCTGAAGAGAG AC	gap	G	SILENT- NONCOD- ING	reductase	Human Gene Homologous to SWISSPROT-ID:16033 NAD(P) DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) • HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)

323	cg43927549	52	CGGTCCGTTGTC CCGGGGGCCAAGCAG apGTTGCAAGCGCT CCCACCCCTCCAGG CG	G	SILENT- NONCOD ING	reductase	Human Gene Homologous to NAUDPH DEHYDROGENASE (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) (HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (spier)
324	cg43947066	780	TTCACAAAGGCT GGGGTATTATATA /GTTAGAACATT CCAAGTGACTCT	A	G	SILENT- NONCOD ING	Human Gene SWISSPROT- ID O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
325	cg43923264	113	AGAAAAGGGGG /AATGGGGCACG /gap/AGAGGGGG GCCTTGATGACCC GC	C	gap	SILENT- NONCOD ING	Human Gene SWISSPROT- ID Q14012 CALCIUM-MODULIN- DEPENDENT PROTEIN KINASE TYPE I (CC2.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
326	cg43942332	1926	AGATCATAGAA TAGGATTITGCA/ CJAATCCACCCA TATCTGTTGAC	A	C	SILENT- NONCOD ING	Human Gene Homologous to SPREMBL-ID:CO00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11

327	cg43274705	580	CGCTGTCTCTGTC TTCGTTTAAAGT TCAGAGAATATA TGGCACGAAAAT	G	T	SILENT- NONCOD- ING	struct	Human Gene Homologous to SPTRM8H1 - ID:Q28891 (MUGCN - BOS TAURUS (BOVINE)), 600 aa (fragment).	4.80E-110	12	
328	cg42207316	146	CCACTCTCCTGGGA CACATGGCTCT TGGTTCTCA ATGCCCTTC	C	T	SILENT- NONCOD- ING	struct	Human Gene Similar to SWISSPROT-ID:P12273 PROLACTIN-INDUCIBLE PROTEIN PRECURSOR (SECRETORY ACTIN-BINDING PROTEIN) (SABP) (GROSS CYSTIC DISEASE FLUID PROTEIN 15) (GCDFP-15) (GP17) - HOMO SAPIENS (HUMAN), 146 aa also: SWISSPROT-ID:P12273 PROLACTIN-INDUCIBLE PROTEIN PRECURSOR (SECRETORY ACTIN-BINDING PROTEIN) (SABP) (GROSS CYSTIC DISEASE FLUID PROTEIN 15) (GCDFP-15) - HOMO SAPIENS (HUMAN), 146 aa.	3.50E-74	7 (7q32)	
329	cg43927885	546	CATGATCATATA GTTTACTACGCA/ TCTTAATCCCG AGAGCTCCCT	A	T	SILENT- NONCOD- ING	struct	Human Gene Similar to SWISSPROT-ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN) AND BOS TAURUS (BOVINE), 15 aa.	1.20E-55	17	

330	cg40388639	5029	CCTTGCCAGGCCG GCTGCAAGTTTgap /TTGTAAGCCGG ACAGACACTGCTG A	T		SILENT- NONCOD- ING	synthase	Human Gene SWISSPROT- ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NITRORADICAL NOS) (NNOS)* HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
331	cg43929316	5355	AGGTAAACAACA GOAATACACACIC /TTCTCTCCCTTT CIOCTCTAGAAAGG	C	T	SILENT- NONCOD- ING	synthase	Human Gene SWISSPROT - ID:PA9651 PHOSPHATIDYL SERINE SYNTHASE (SERINE- EXCHANGE ENZYME) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 173 aa.	9.80E-269	8
332	cg43958714	1563	TGGGTGATGATCA CGTGTCTGCTGTT CIGGCTCATGGCAG AGCATTAGTCCC	T	C	SILENT- NONCOD- ING	synthase	Human Gene Similar to SPTR04BL-ID:Q42761 SQUALENE SYNTHASE (EC 2.5.1.21) (FARNESYL- DIPHOSPHATE FARNESYLTRANSFERASE) (FARNESYLTRANSFERASE) (PRESQUALENE-DI- DIPHOSPHOPHATE SYNTHASE) * GLYCERPHOSPHATE GLABRA, 412 aa.	9.20E-83	8

333	cg43275028	2508	ACAGACTGGCTC AGCATTAAGAATIC TTAGGTCAATTCGGA AACTCATCATGAA	C	T	SILENT- NONCOD- ING	synthase	Human Gene Similar to SWISSPROT-ID:70490 MILK FAT GLLOBULE-EGF FACTOR 8 PRECURSOR (MFG-8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM)- RATTUS NORVEGICUS (RAT), 427 aa;iplets:SPTRNBL- ID:70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
334	cg43275028	2335	GOTATTCGGAAA CTCATTCATTGAAIT CICAGGAAAGAA AGAGTTCAATCTT A	T	C	SILENT- NONCOD- ING	synthase	Human Gene Similar to SWISSPROT-ID:70490 MILK FAT GLLOBULE-EGF FACTOR 8 PRECURSOR (MFG-8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM)- RATTUS NORVEGICUS (RAT), 427 aa;iplets:SPTRNBL- ID:70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)

335	cg43275028	2601	AQAATGGCACTGA ATTGTTTCTTCIA/ GAAACAGAAATA ATTGTTGGTCAA	A	G	SILENT- NONCOD- ING	synthase	Human Gene Similar to SWISSPROT-1D-P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM)- RATITUS NORVEGICUS (RAT), 427 aa [pcklSPTRMBL- ID-P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE- RATITUS NORVEGICUS (RAT), 427 aa]	3.20E-65	I (1q23)
336	cg43275028	2873	CCTTCACTTGTGCG TGAGGAATTCA/A G/AAGTCAAAAC ATGCTAAAGCATAA G	A	G	SILENT- NONCOD- ING	synthase	Human Gene Similar to SWISSPROT-1D-P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM)- RATITUS NORVEGICUS (RAT), 427 aa [pcklSPTRMBL- ID-P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE- RATITUS NORVEGICUS (RAT), 427 aa]	3.20E-65	I (1q23)

337	cg43275028	2894	TICAAAAGTCAG AACATGCTAAGCTA /GTTAAGGGACCCA AGGTAGAAAAAGAGA T	A	G	SILENT- NONCOD- ING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM)- RATTUS NORVEGICUS (RAT), 427 aa.[poly]SPTRMNL- ID:P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	I (1q23)
338	cg43275028	3073	TTCCTTCAGAA TGAGCCCTGGAA GAGGACCCCTCTA GTGATCTCTTACT	A	G	SILENT- NONCOD- ING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM)- RATTUS NORVEGICUS (RAT), 427 aa.[poly]SPTRMNL- ID:P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	I (1q23)

339	cig43275028	5590	ACTACATAAGGAC AGCAACATGCC/TIA /GTTGGACATAGAA GAATTTCCTTA	A	G	SILENT- NONCOD ING	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GLY GANGLIOSIDE SYNTHASE) (AGS) (MFGM)- RATUS NORVEGICUS (RAT), 427 aa, 427 aa, ID: P70490 O-ACETYL GD3 GANGLIOSIDE SYNTHASE- RATUS NORVEGICUS (RAT), 427 aa.	3'20E-65	1 (1q23)
340	cig43985000	1856	GAAGAAATATACA AGGCAAACGTGAACT /GTCGGGGAACT CTTCTCTGATCCCT	C	G	SILENT- NONCOD ING	tm7	Human Gene SWISSPROT- ID: P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.50E-236	4
341	cig3955524	1684	TCCGACCCACAC ACCGTGAAGAAC /GJCCCTACCTAGCC TCAGCCCTCTCTG	C	G	SILENT- NONCOD ING	tm7	Human Gene SWISSPROT- ID: P157572X PURINORECEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
342	cig43306266	1503	ATAATCCATGCCCT TGAATATTAGAATV /GTTGGTTCTTGAA TGGGATTTGAAT	T	G	SILENT- NONCOD ING	tm7	Human Gene SWISSPROT- ID: P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EF3 RECEPTOR) (PGE RECEPTOR, EF3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

343	cg43306266	1641	GGGATTGATA TGCAATTAAAGAAG apCGITGGGAGA ATTTCACAGATGA TG	gap	C	SILENT- NONCOD ING	tm^7	Human Gene SWISSPROT- ID: P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	I (1p31.2)
344	cg43306266	1650	GAATATGGATTA AGAAAGTTGGAAI GICJAATTCAACAG ATGTGATGGAG GA	G	C	SILENT- NONCOD ING	tm^7	Human Gene SWISSPROT- ID: P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	I (1p31.2)

345	cg43329467	683	TCGGCAAAATCTTG AAAAGTGGGGQI CTTGACAGAGACAT GGATGTGACTCC CA	C	T	SILENT- NONCOD ING	tm ⁷	Human Gene SWISSPROT- ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL-8- RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN- COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) (OPCR-BR) • HOMO SAPIENS (HUMAN), 375 aa [pols]SWISSPROT- ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL-8- RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN- COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) -HOMO SAPIENS (HUMAN), 375 aa [pols]TREMBL NEW- ID:62456121 G-PROTEIN COUPLED RECEPTOR- HOMO SAPIENS (HUMAN), 375 aa	8.20E-201	X
346	cg2751286	439	AAGGGATAAGAAC ggp	G	G	SILENT- NONCOD ING	tm ⁷	Human Gene SWISSPROT- ID:62456122 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2)-HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X

347	cg11751407	76	GAATGTGGGATA AGCATTTGGGAC/C /TCTATCAGGATTC CTGAGGAGAAGCT	C	T	SILENT- NONCOD ING	tm ⁷	Human Gene SWISSPROT- ID:146069 PROBABLE G- PROTEIN-COUPLED RECEPTOR GPR1 (ACCA ORPHAN RECEPTOR - HOMO SAPIENS (HUMAN), 350 aa.	3.20E-176	1
348	cg43326635	135	CAGCGGGAACTC TGCCAGCTTGGC/C TJAAGGAGGAGTG CTTCCCTCTGCC	C	T	SILENT- NONCOD ING	tm ⁷	Human Gene SWISSPROT- ID:PF0542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
349	cg43326635	139	CGGGAGCTCTCC AGCTTTGGCGAAG /CAGGGGTGGCTG CCTGGTCCCCTTG	G	C	SILENT- NONCOD ING	tm ⁷	Human Gene SWISSPROT- ID:PF0542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
350	cg43993798	1839	TGCCTCTGGCTGTG ATGGAGGAGGA/A/ GIGGGTGGATCC GTGGAGCTCAA	A	G	SILENT- NONCOD ING	tm ⁷	Human Gene Homologous to SWISSPROT-ID:P31421 METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR - RATTUS NORVEGICUS (R.A.T.), 872 aa.	6.90E-109	3 (3q21)

351	cg45040271	2130	ATGCTCCCAAC CCTAGGGATC/ CIAACTTAAAGATA ATTGCCACTCT	A	C	SILENT- NONCOD- ING	tm7	Human Gene Similar to SWISSPROT-ID-Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-L-LOC 2)- LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa SwissProt:SPTRMBL-ID-Q25322 GC2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.90E-74	
352	cg45040271	2139	CCAACCTAGGA ATCAACATTAAG /TAAATTCAC TTCTCCTCTCT	G	T	SILENT- NONCOD- ING	tm	Human Gene Similar to SWISSPROT-ID-Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-L-LOC 2)- LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa SwissProt:SPTRMBL-ID-Q25322 GC2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.90E-74	

353	cg434040271	2163	AGATAATGCCA CTTCCTCTTTC TCACGGTTGAG	C	T	SILENT- NONCOD- ING	tm7	Human Gene Similar to SWISSPROT-ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2)- LOCUSTA MIGRATORIA (MIGRATOR LOCUS), 484 aa.[PDB:SEPTREMBl-1D;Q25322] GCR (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUS), 484 aa.	2.90E-74
354	cg434040273	1668	CCTAGAGCCCGC CTTGCTGCCCTT CJGCTGAGGCC CCAGCCAATGCGC	T	C	SILENT- NONCOD- ING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58
355	cg434040273	1760	CAGCGCTTGTCA TGCGACCCAAAT GGAAGCCATGGC CGGACCAAGCT	A	G	SILENT- NONCOD- ING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58
356	cg434040273	1793	TGGCGGGACAC GACGTCACGAGAC KIAAAGGGAGAG GTGTGGGTGTTGG	C	G	SILENT- NONCOD- ING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58

357	cg43040273	2767	GCGAGTCCTCTTCTTG AAGGCCATATTG/G CIAATGCGCTACTCC AGCAACGGCAACA	G	C	SILENT- NONCOD ING	tmt7	Human Gene Similar to SWISSPROT-ID-Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
358	cg43040273	2953	ATTTAGTACAAA TGACTCTACTCTG/ ATAAACAGCAGTT TCTACCTTAAAG	G	A	SILENT- NONCOD ING	tmt7	Human Gene Similar to SWISSPROT-ID-Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
359	cg43040273	3053	ATAAACCTTAAGAT AAAATTGTTAAAGA AG/ATACTGTATAG ATACTGACAGAGA AG	gtt	A	SILENT- NONCOD ING	tmt7	Human Gene Similar to SWISSPROT-ID-Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
360	cg43986970	1501	AGGGTTGGAAGTG CTGATGGGATTG/A PTTCCTCATTCCT TTCGTATAAAGGT A	gtt	T	SILENT- NONCOD ING	transcriptfactor	Human Gene SPTRMBL- ID-Q07279 TRANSCRIPTION FACTOR NF-E2 • MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12
361	cg43986970	249	AGCCCTCCAGAG ACAACACGGGA G/C/C/CATCTCTC TCCTCA CCTGCTG	G	C	SILENT- NONCOD ING	transcriptfactor	Human Gene SPTRMBL- ID-Q07279 TRANSCRIPTION FACTOR NF-E2 • MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12

362	cg43947199	2623	GTCTCTCCGGCC CAACCGCTGAGCT TAAGGGAAATGG GCGAACGTCGAGC	T	SILENT- NONCOD ING	Transcripfactor ID: P2193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) HOMO SAPIENS (HUMAN), 301 aa;Ref SWISSPROT-ID:P2193	Human Gene SWISSPROT- ID:P2193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
363	cg43917396	934	GGGGGGGGGGCACT GCCCAAGGAAGGGG A/GCTCCGGAGAA GGGAGCCGCGCGC TG	A	SILENT- NONCOD ING	Transcripfactor ID: C29210821 TRANSCRIPTION FACTOR T- BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	Human Gene Similar to TRIMBLINE-ID:C29210821 TRANSCRIPTION FACTOR T- BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
364	cg40351913	2030	AGACGAAGAGCC AGAAAGTCACTCT /CIGCAATGAGA GACACGAAACAAAC C	C	SILENT- NONCOD ING	transport ID:Q01959 SODIUM- DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	Human Gene SWISSPROT- ID:Q01959 SODIUM- DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (Sp15.3)
365	cg43921289	237	CCCACGGCTGCCA GGAGCAAGCGGAG ATGAGCCAGCGG GCCGGCGCACTCG GA	A	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene SWISSPROT- AC: P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

366	cg43928515	3196	AAACAAATAAGCC CTTTTACTGAC/A/ GATGCAACCAACC TTTCAGGTGAAG	A	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa. (fragment).	0	16
367	cg43955093	1309	AGAGCUAAAATC CAAGTTGGATT/C/ GTTAAGCAGCTTG ACAGTAATCTTG	C	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1159 aa.	0	16
368	cg43955093	1336	AAGCAGCGCTGAC ACTAAATCACTGAA /GTTGGTAGGGAAA AAAAGAACATGG G	A	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1159 aa.	0	16
369	cg43923474	2206	AGGCCAAAGCTCA /CICCGAAAAGGG GCCTAAAGTGAAAG T	A	C	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-IP PROTEIN) - Homo sapiens (Human), 396 aa.	0	1 (fp32)
370	cg44014437	4893	CIGCTCCANCTTC GCCAGGCTCA/A/ GTTGTTAACCTCC GGGTGTTAGTGGC	A	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC:P53675 CLATHRIN HE/VY CHAIN 2 (CLH-22) • Homo sapiens (Human), 1640 aa.	0	17 (17q11)

371	cg4014448	5114	CTGCTCCACAACTTC GCCAGCCTCA/A GTTGACAACCTCC GCGTGTAGGGC	A	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC:P51675 CLATHRIN HEAVY CHAIN 2 (CLH-22) - Homo sapiens (Human), 1640 aa.	0	17 (17q11)
372	cg43973129	2242	CACTCACGAAA GACACATTATTC/ ATTAACCAAGGGCA GAAACTGAACTT	C	A	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC:P05060 SECRETOGRAININ (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa.	0	20 (20q1ter)
373	cg43950637	1939	GATAAGGACTCAAG CTTATTTGGGATTC TGTGATCAATTCT TCTGATGTTGTT	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC:Q13099 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0	21 (21q22.1)
374	cg43956384	2416	TACAGCCATCTGT ATCTACTGGACIC TGCGAGAAGGAA GTCCACCTCACTCA C	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC:P13866 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM/GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 664 aa.	0	22 (22q13.1)

375	cg3992229	101	AGCA GTGCA GGC CGCC CGC GRAGCA GA TGG AGCTCG CCC GGCG CCGGG CC	G	A	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene SWISSPROT- AC:P2332 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE-LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)
376	cg4932392	260	GAGAAAAAGCATG GTACCCAACCGAIA TTTTCACHTTC AGCAATCTAC	A	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene TREMBL NEW- AC:AA2358I CULIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
377	cg4932392	323	TAAGTTTAAAGA AAATGCTATAATGIA /TICATGACTGTA AAATATCTCTAGGC A	A	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene TREMBL NEW- AC:AA2358I CULIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
378	cg3981656	1121	AGCAAAGAAACAC TGGCAAAATCCIA /TGCATTGCAAA ATTCTAAAGTTGG	A	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene TREMBL NEW- AC:CAAA08974 GLUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1,60E-292	10
379	cg4910613	366	AAATAAATGTTTCT ATAGTCATTACTA CTTACAATGGGA GIGCTAAATTC	T	A	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene SWISSPROT- AC:P38567 HYALURONIDASE PRECURSOR (EC 3.2.1.35) (SPERM SURFACE PROTEIN PH-20) (SPERM ADHESION MOLECULE 1) - Homo sapiens (Human), 509 aa.	1,20E-280	7

380	cg44035104	1189	AACTGGGTTGCTCT AAGAACGTATTC CCTAAACCTCTC AGCATGGCGTGA	T	C	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP37287 N- ACETYLGLUCOSAMINYL- PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN (GLCNAC-PI SYNTHESIS PROTEIN) (PHOSPHATIDYLINOSITOL GLYCAN COMPLEMENTATION CLASS A) (PfG-A) - Homo sapiens (Human), 484 aa.	4.70E-261 (X (Np22.1)	
381	cg43929959	1643	CAATGATGATTC TGACCCCTGGGG GGTAAGGCACCTCAC ATGCCGCCAG C	G	Gap	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP7806 DIABETES MELLITUS TYPE I AUTOANTIGEN (ISLET CELL AUTOANTIGEN 169) HOMO SAPIENS (HUMAN), 463 aa.	2.10E-288 7	
382	cg43950250	1961	TGTGATGATTC TTGATGTTCTC GAACT TTAAATGAAACT AAGAGATGGAATT	C	Gap	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP11926 ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC) - Homo sapiens (Human), 461 aa.	7.00E-251 2 (2p5)	
383	cg43064090	129	GCGGAGTCCTCGTG GTGGGGCGAACGGA TTAGGGGAGAGC CAGTAGGGAGAGT G	A	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP32754-4- HYDROXYPHENYL PYRUVATE dioxygenase (EC 1.13.11.27) (4HPPD) (HPD) - Homo sapiens (Human), 392 aa.	4.80E-213	

384	cg43064090	130	CCGAGTCCTCTGG TGCGGAGACCCAA T/GGGGAAGAGGCC AGTAGGGAAAGTTG G	A	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC232754-4- HYDROXYPHENYL PYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD) (4HPPD) - Homo sapiens (Human), 392 aa.	4.80E-213
385	cg43064090	137	GGGAGCAGCCAGT AGGGAGTGTGGI C/GAGTTCAGA ATAGGGGGCTG GC	C	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC232754-4- HYDROXYPHENYL PYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD) (4HPPD) - Homo sapiens (Human), 392 aa.	4.80E-213
386	cg43064090	61	TAATGGGGGC TOAGCAGAGGGI C/GGCCCGCCG AGGGGGTGTCA GT	C	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC232754-4- HYDROXYPHENYL PYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD) (4HPPD) - Homo sapiens (Human), 392 aa.	4.80E-213
387	cg430460224	32956	GATGCCAAAAAA CAAAGTGTGAAAT AC/TCCACAAACACA GTCATAAACCTAG CA	A	C	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC230968 GONADOTROPIN- RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 323 aa.	1.20E-177
388	cg43924431	381	GUCUUTACAGATG T TTTCAAAATG AGAGTTCAGTA AAATATTCAATT	T	gap	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC:Q16637 SURVIVAL- MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.20E-166

389	cg13936047	607	CGTTTCTCATATG TGATCTACACATC GCCGTGTCATC GAGATTCGGTC	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene TREMBL NEW- AC:AD40550 P38P - HOMO SAPIENS (HUMAN), 733 aa.	4.30E-164	13
390	cg13272443	1542	TGGGATTACAGGT GGCACTACACIA /GJCAAGCTTAATT TGTATTTTGTAG	A	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC:CP13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) CD142 (ANTIGEN) • Homo sapiens (Human), 295 aa.	7.70E-158	1 (p22)
391	cg13966848	2065	CCTCTAGAACCCCT GCAGCGAAAC/T TAAATGACGCCCG TAGCCGCCATCCG	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene SWISSPROT- AC:Q92600 PROTEIN INVOLVED IN SEXUAL DEVELOPMENT, COMPLETE CDS, HOMO SAPIENS (HUMAN), 299 aa.	4.90E-156	2
392	cg13966140	176	AAAAAGCTACAGA /AAGAAATACATT /CTGAAAMACACA ATGACTCTAGAGC A	T	C	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Homologous to TREMBL NEW-ACC:ZAC6999 SACN21 • MUS MUSCULUS (MOUSE), 721 aa.	1.10E-150	6
393	cg13283114	418	CAGGGACATGGGG /GCAACCCGGGG /gap/CTTGTGGGC TCACAGGACAAATG G	G	gap	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Homologous to TREMBL NEW-ACC:ZAD23440 LR8 • HOMO SAPIENS (HUMAN), 270 aa.	1.90E-138	7

394	cg43948566	370	GCAGGCAAGGCCAC CCTGGACCCAG /mpGGCAAGAGGA CCCCCTGCCCTCCAG T	G	Epip	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Homologous to SWISSNEW-ACC:p18382 CD81 ANTIGEN (26 KD CELL SURFACE PROTEIN TAPA-1) Homo sapiens (Human), 226 aa.	3.30E-125	11
395	cg4403626	619	TAAACAGCCTCACT TCAGGGACTGGTTA /GTACAAAGCTGCG CACCCATCTCAGC C	A	G	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Homologous to SPTRIMBL-ACC:Q1525 mRNA (1652) FOR ORF: PARTIAL CD8 - HOMO SAPIENS (HUMAN), 296 aa (fragment).	2.70E-123	
396	cg43917206	259	TTACAGGACATCA CCTGCCATCTTATV AIGGTTAAATT ACAAATGCTAGT	T	A	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Homologous to SWISSPROT-ACC:P22061 PROTEIN-L-SOASPARTATE(D- ASPARTATE)-C- METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN-BETA- ASPARTATE METHYLTRANSFERASE) PROTEIN(L- ISOASPARTYL-D-ASPARTYL METHYLTRANSFERASE) (L- ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) Homo sapiens (Human), 226 aa.	6.90E-118	6

397	cg43289666	215	GCCGGATTTTCCA CAATTAAATGCT TGAGTCACCTGT ATCCAGCTACAG	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Homologous to SPTREMBL-ACC-000539 CANCER ASSOCIATED SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 213 aa.	2.50E-111	8
398	cg43986282	840	GTTTCAACCCTCC AGACAGGCGATTC TTCAGGGAGGC GGGAGCACCTAAC	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Homologous to SPTREMBL-ACC-P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-10	12
399	cg43986282	841	TITCCACCTCCCA GACAGGCATTC TGAATGGAGGC GGGAGCACCTAAC	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Homologous to SPTREMBL-ACC-P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-10	12
400	cg43297716	1030	CTAAACCCAAATG GGGGCTGGCGCA TTGACCCGGAGG TGCCCTGGCGCACTC	A	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC21518 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA- DERIVED LPL INHIBITOR) (MLPL) - Homo sapiens (Human), 202 aa.	1.20E-106	22 (22q12.1)

401	cg43980312	2160	TITATCAITAAAG TGCCAGAATGGC TTCITTAATGAA ACAAAAAACAAA	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN-2 PRECURSOR (Heparan Sulfate Proteoglycan- Core Protein) (HSQC) (SYNU2) - Homo sapiens (Human), 201 aa.	7.90E-101	8 (8q22)
402	cg43939240	624	GGAGGTGGAGT /TGAAGCGGCA GGCCCCATGCAAAG G	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SPREMB1,-ACC:Q43399 HD44-INS2 ISOFORM-1-HOMO SAPENS (HUMAN), 206 aa.	1.00E-100	
403	cg43941552	881	GCCACCTGGCGG GCTGTGAGAAG[C /gap]GCTCCGCTG ACCAAGCCCTGG GC	C	gap	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:P1186 PULMONARY SURFACTANT- ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAI)) - Homo sapiens (Human), 197 aa.	1.60E-100	
404	cg43941552	1124	GCTTCCTGCCACAC CGCAAGGACAAAV GICCTGAGAAAT GGAGCTGCGGA	A	G	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:P1186 PULMONARY SURFACTANT- ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAI)) - Homo sapiens (Human), 197 aa.	1.60E-100	

405	cg42917153	914	CATTCCTCTTGTAA CATAAATCATTGTT AACCTCCCTGGCT CTCTCCCTTCTCA	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:249973 PROTEIN 1 HOMOLOG ALPHA (HPI ALPHA) (ANTIGEN P25)- Homo sapiens (Human), 191 aa.	2.10E-100	12
406	cg43927693	878	CAGGGGTCAAGAG AGCTCAGAGTG TGCCCCACCTGA GCCCAACCGG A	G	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:23056 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.30E-95	22
407	cg43951338	507	CAGAAAGCAGCAA ATTAGTTTTCA AAGGACCGAATT GGCTCCGAGCT	C	A	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:236405 ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.40E-93	10
408	cg43951338	511	AAGCAGCAAAATA GTGTTTCAAGGA/ CUCGAAATTGGCT CCCGAGCTCTG	A	C	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:236405 ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.40E-93	10
409	cg43951338	547	CTCCGGAGGCTCT GAGTCCTCAATTCT GGCTAGATTTAT TCTCTCTGCA	C	T	SILENT- NONCOD- ING	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:236405 ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.40E-93	10

410	c223236776	1234	CCCGCCAGGCC ACGCTTACTAGTG ap/TCCCCGGGGC GCCCAACGGGC GC	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSNEW-ACC-P0185 VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91	
411	c223236776	1240	CCAGCCGAGCOC TACTGAGCCOGIC /TGTCTGCCAAC GGCGGCTCTTCG	C	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSNEW-ACC-P0185 VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91
412	c223236776	1242	AGCCCGAGCCTA CTAGGCCCGCGC /TTGGCCCAACGG CCGGCTCTCCG	C	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSNEW-ACC-P0185 VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91
413	c223236776	1246	CGACGCCCTACTGA GCCCGGGCGCTGC /TCCCACGGCGC GCTTGTGCCCG	C	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSNEW-ACC-P0185 VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91

414	cg439768406	1362	GCTACGTTTACTCA CAGCCAGGA[ga] [a]ACTGACATAAA ATAACTAACAAAC A	A	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to REMTREMBL-ACCE:47283 DNA FOR ORF1 AND ORF2 FROM CHROMOSOME X- HOMO SAPIENS (HUMAN), 157 aa.	5.00E-83 X (Xp11.4)
415	cg42748586	104	CGCCCTCTGATCCA AGCCACCTCGTC[G /T]CAGAGGGTGT CATGGCTTCCAA A	C	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSNEW-ACCP01258 CALCITONIN PRECURSOR - Homo sapiens (Human), 141 aa. (1p15.2)
416	cg43959533	336	CTCTGACAAGGG AA[GCTTCTTA]T [gap]TTTTTTCT TTGCGAAAACAGA	T	[gap]	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to TREMBLNEW-ACCAAD39844 HSPC23 - HOMO SAPIENS (HUMAN), 419 aa.
417	cg43976681	1119	AATGGCTCAAGTC AGTGACCCAAAGG A[gap]ACCTTCAG AATGGATGAATA GAC	A	[gap]	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to TREMBLNEW-ACCAAD39427 MYONEGALIN - RATTUS NORVEGICUS (RAT), 2324 aa.
418	cg43976681	1120	A[TGGCTCAAGTC GTGACCCAAAGG] A[gap]CCTTCAGA ATGGATGAATA ACC	A	[gap]	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to TREMBLNEW-ACCAAD39427 MYONEGALIN - RATTUS NORVEGICUS (RAT), 2324 aa.

419	cg4394044	714	CCAAAGGGAGGC CATTTCCTGTC/C/ TICITCCCTGAGTG TCCGGGGGGGGG	C	T	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSPROT-ACC-00455 TTF-I INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment).	7.30E-66	19
420	cg43933283	398	CATAATGGCGA ATTTCAGGATTG/ AGGAGAAAGAT GCTCCCTTCAGCC	G	A	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSPROT-ACC-006062 FRUCTOSE-BISPHOSPHATE ALDOLASE B (EC 4.1.2.13) (LIVER-TYPE ALDOLASE) • Homo sapiens (Human), 363 aa.	6.60E-65	9 (922)
421	cg42381630	577	AAAGCAATACAG TOTAAAAAGAACIG /AICAGTTGAAT GATGAGGTGT C	G	A	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSPROT-ACC-076087 GAGE-8 - HOMO SAIEENS (HUMAN), 117 aa.	5.90E-64	
422	cg41664708	423	CCAGGCCAGGTCA TTCATTTAAC/G/ C/CATGGACTGAA GTTTATACTAAC	G	C	SILENT- NONCOD ING	UNCLASSIFI ED	Human Gene Similar to SWISSPROT-ACC-P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1) ALPHA • Homo sapiens (Human), 114 aa.	2.00E-54	1

423	cg43277652	3906	AGCCCTCCGAG AAAAGATCAGI CTCCCCAGAACCT TCTCTGTCTGATT	C	T	Ala (652)	CONSER VATIVE	ATPase associat ed	Human Gene SWISSPROT- ID:P35670 COPPER- TRANSPORTING ATPASE 2 (EC 3.6.3.6) (COPPER PUMP 2) (NILSON DISEASE- ASSOCIATED PROTEIN)- HOMO SAPIENS (HUMAN), 1465 aa.	0	¹³ (13q14.3)
424	cg4310734	1138	TACCAAGGGCTGC ATCGGCTGGCGIC /GAGGAGCATGCG CGTCGTTATTGGG	C	G	Ala (653)	CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:PO6514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1IB) (INTEGRIN ALPHA-1B) (CD41) -HOMO SAPIENS (HUMAN), 1039 aa.	0	¹⁷ (17q21.3)
425	cg4310734	1238	TGGGGGGCGCTCC ACTGATAATGAG /CAGCCGGCGAA CGAAAAACTGGCC G	G	C	Glu (654)	CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:PO6514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1IB) (INTEGRIN ALPHA-1B) (CD41) -HOMO SAPIENS (HUMAN), 1039 aa.	0	¹⁷ (17q21.3)
426	cg4310734	1893	CTCTCAACAGCCA GGCACCACTCTGA /GACCTGATCTG GGCGAAACACA G	A	G	Asn (655)	CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:PO6514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1IB) (INTEGRIN ALPHA-1B) (CD41) -HOMO SAPIENS (HUMAN), 1039 aa.	0	¹⁷ (17q21.3)

427	cg43982507	1883	GGTACAGGTGAA AATGATGTTGTCG /CCTATCAAATGG ATCTTGCTACTGGC	G	C	Gly	Ala (656)	CONSER- VATIVE	eph	Human Gene SWISSPROT- ID:P98135 VERY LOW- DENSITY LIPOPROTEIN (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (p24)
428	cg41554010	949	GCGGAGGAGGCG /TGCGCAACTCTAAG /AIGGGCAACACCG AGGGGTGCGAGAA G	G	A	Arg	Lys (657)	CONSER- VATIVE	eph	Human Gene SWISSPROT- ID:P06727 APOLIPOPROTEIN A- IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa; SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) HOMO SAPIENS (HUMAN), 396 aa.	1,80E+203	11 (11q23)
429	cg43299024	1036	TACAGGGGGCCCT TGGAGACCCCGGIA /GTTGCCACAGCC GGCACCGCCCC A	A	G	His	Arg (658)	CONSER- VATIVE	glucosidase	Human Gene TREMBL NEW- ID:G2R26521 MALTASE- GLICOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1837 aa.	7.40E-199	17 (17q25.2)
430	cg43299024	1108	GAGGAAGCCCTCG GGGTGATGCTGCG /GICCGGCACTCTG AGGGCCGCGCTGT G	A	G	His	Arg (659)	CONSER- VATIVE	glucosidase	Human Gene TREMBL NEW- ID:G2R26521 MALTASE- GLICOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1837 aa.	7.40E-199	17 (17q25.2)

431	cg42365373	12840	GAATGACTTGGGAA AAGGAACTAAAT ACITCGAACTCC TGGATGAAATGGAG A	A	C	Ile (660)	Lys (CONSER VATIVE)	Glycoprotein	Human Gene SWISSPROT- ID P98164 LOW-DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN 2 (MEGALIN) GLYCOPROTEIN 330 aa - HOMO SAPIENS (HUMAN), 1751 aa (fragment).	0	2
432	cg36834323	1004	AGTTATTCAGAG GATACAGAAATCA /GTCGAAGTCCC GAGAAAATGGGA G	A	G	His (661)	Arg (661)	Glycoprotein	Human Gene Similar to SWISSPROT-ID P238159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRN P G) GLYCOPROTEIN P43 - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
433	cg41538631	2101	GGACCAAGGGGCC ATGCTGTCTCATIG/ ATCTAGGGCAC TCAGGAGAGCG	G	A	Val (662)	Ile (662)	Glycoprotein	Human Gene Similar to SWISSPROT-ID P16432 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q1.2)
434	cg42359555	666	TGCTTTCAGGGCG GAAAACCTCTTA GTTGTCCTGGAG CTGAAGATACTCC	A	G	Ile (663)	Val (663)	Glycoprotein	Human Gene SWISSPROT- ID P09848 LACTASE PHORIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE; GLYCOSYL CERAMIDASE)* HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q11)

435	cg43998672	1331	GIGTGCGCCATTG TAAACTCTAGCAIC /AIGCGCGCTATGTC CTCCCTGGTTGGTC	C	A	Val (664)	Leu (664)	CONSER VATIVE	hydroxysteroid	Human Gene SPTRMBL- ID:Q13194 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220 (16q22)	16 (16q22)
436	cg43969028	1133	G6AGATGGGGTCA TTCCTAGTGTATTA TITTCAGATAGT GGGAGGAACCAAC	A	T	Tyr (665)	Phe (665)	CONSER VATIVE	immunoglob	Human Gene Homologous to SPTRMBL ID:PM456 SIMILAR TO THE IMMUNOGLOBULIN SUPERFAMILY - CENORHABDITS ELEGANS, 1173 aa.	2.20E-149 (18q21.3)	18 (18q21.3)

437	cg45933479	133	AAGGAGAAGAGAA ACGTGTTATCCGA GTTCCATGGTGA AGGTACAATAAT	A	G	His (66)	Arg CONSER ATIVE	interleukin	Human Gene SWISSPROT- ID: P29466 INTERLEUKIN-1 BETA CONVERTASE PRECURSOR (IL-1RC) (EC 3.4.22.36) (IL-1 BETA CONVERTING ENZYME) (ICE) (INTERLEUKIN-1 BETA CONVERTING ENZYME) (P45) (CASPASE-1) (CASP-1)- HOMO SAPIENS (HUMAN), 404 aa;RefSeq:SWISSPROT:IP29466 INTERLEUKIN-1 BETA CONVERTASE PRECURSOR (IL-1BC) (EC 3.4.22.36) (IL-1 BETA CONVERTING ENZYME) (ICE) (INTERLEUKIN-1 BETA CONVERTING ENZYME) (P45) (CASPASE-1) (CASP-1)- HOMO SAPIENS (HUMAN), 404 aa.	2.50E-206	
438	cg45942537	1163		C	A	Val (667)	Leu CONSER ATIVE	kinesin	Human Gene SWISSPROT- ID: P3176 KINESIN HEAVY CHAIN (UBQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa;RefSeq:SWISSPROT:IP3176 KINESIN HEAVY CHAIN (UBQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0	10

439	cg33337333	1035	TTC G /ATCTCCTGCCAT GAGCACCAAGTC	G	A	Val (668)	CONSER ATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK (HUMAN), 455 aa.	1.80E-113	19
440	cg33337333	271	CTGGAAACAGATTC CTCATTTAGGCCCT(G CTGACCCAGCAC AGCGAGGAACTA	G	C	Val (669)	CONSER ATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK (HUMAN), 455 aa.	1.80E-113	19
441	cg33337333	823	TCATCGCTGTGCT CCA GJATGCCTGCTTA TGA ACCAAGGCC	A	G	Asn (670)	CONSER ATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK (HUMAN), 455 aa.	1.80E-113	19
442	cg30421838	3434	GGATCGCTGTGCTC TC ATG ATGAAAGCCAAAGC	G	T	Val (671)	CONSER ATIVE	nuc. recept	Human Gene SWISSPROT- ID:PG6401 PROGESTERONE RECEPTOR (PR)- HOMO SAPIENS (HUMAN), 933 aa SwissProt ID:PG6401 PROGESTERONE RECEPTOR (PR)- HOMO SAPIENS (HUMAN), 933 aa.	0	11 (1q2)

443	cg43046060	1019	GCCATGGCATCC AGAACAAAGGAGGI CTTGGAGTCGCC AATCTTCACTGCTG C	C	T	Ala (672)	CONSER VATIVE	nucl_recept	Human Gene SWISSPROT- ID:Q07869 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR- ALPHA) -HOMO SAPIENS (HUMAN), 468 aa [ppkesPTREMBL-ID:Q16241] PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA -HOMO SAPIENS (HUMAN), 468 aa (fragment).	4.10E-244	22
444	cg4391813	1860	TCTGACATACAG CATTCCAAAGATT CIGGAGGAATTT GTCCACGCTGAG	T	C	Le (673)	CONSER VATIVE	nuclease	Human Gene SWISSPROT- ID:Q46922 MUTL PROTEIN HOMOLOG 1 (DNA MISMATCH REPAIR PROTEIN MLH1)* -HOMO SAPIENS (HUMAN), 756 aa.	0	3 (3p21.3)
445	cg43904626	194	GAGTGCCTGACG ATACAGCTTAATTC/ GJAGAAATCAATTG TGGAAGAAATGA	C	G	Gln (674)	CONSER VATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:POL118 TRANSFORMING PROTEIN P21K-RAS 2B -HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12
446	cg42904626	548	AAGAGATTAGGA ATTCCCTTTATTC/G C/AACATAGCCA AGACAAAGACAGGG	G	C	Glu (675)	CONSER VATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:POL118 TRANSFORMING PROTEIN P21K-RAS 2B -HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12

447	rs4246457	2845	GCGCCTACCCA GCAAGAAGGGC CTTAGGCCAGTCC TAGGCCACACAGA G	C	T	Ala (676)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT- ID:P22470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP-GAMMA)-HOMO SAPIENS (HUMAN), 1445 aa.	0	³ (3414.2)
448	rs43272394	582	GGATGTACTGCA TTGTTCTCTGTT CIGCTATGTCGA GGCAAGACTCTGT	T	C	Val (677)	CONSER VATIVE	phosphatase	Human Gene Similar to SPTRIMBL-ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa.	1.40E-79	19
449	cg43938858	807	TCAAGGTTGGGA ACCTACCGTGTC GTTCTCGAAAGA AGGAGGCTACAC	C	G	Lys (678)	CONSER VATIVE	polymerase	Human Gene SWISSNEW- ID:P22205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHAI HOLOENZYME-ASSOCIATED PROTEIN P1) (RPLB BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa Human Gene SWISSPROT-ID:P22205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHAI HOLOENZYME-ASSOCIATED PROTEIN P1) (RPLB BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa	0	⁶ (6p12)

450	cg43916732	540	GTACAGGGGGGG GCCACTCGGGCA /TCTGAGCACAA TTTGGGGGGC G	A	T	Thr (679)	CONSER VATIVE	protease	Human Gene SPTREMBL- ID:Q15113 PROCOLLAGEN C- PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1:20E-247 (7q21.3)	7
451	cg42894809	2745	GGATGCCGGAGAG TGGATCACTCTCA GJATCAGACACAA ACAGCCAAACGTT A	A	G	Asn (680)	CONSER VATIVE	struct	Human Gene SWISSPROT- ID:IP54226 M-PROTEIN (165 KD TISSUE-ASSOCIATED PROTEIN) (165 KD CONNECTIN- ASSOCIATED PROTEIN)- HOMO SAPIENS (HUMAN), 1465 aa.	0	8
452	cg40388639	2337	GATTCTCTAGAG CTGGTGTGAAAG /CUTTCATAGGC ACCCAAAGTTGA	G	C	Val (681)	CONSER VATIVE	synthase	Human Gene SWISSPROT- ID:IP29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS)- HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
453	cg40388639	2380	AAGTTGAGGGT TCAAGGAACTGG /CAGCTGAGTGT ACGGGCTCCGG C	G	C	Gly (682)	CONSER VATIVE	synthase	Human Gene SWISSPROT- ID:IP29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS)- HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)

454	cg43124627	1524	AATTCTATACAC TGGGACAGAGC GATATATGATAA AGATGGTATTTC	C	G	Ala	Gly (683)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa RefSeq:SWISSPROT-1D:P39062	7.7E-79	16	
455	cg43124627	869	TGGAAACAAGTGGAA TATCGAAAATGAA TTCTGCACACACCC ACAGCAAGTTGG	A	T	Thr	Ser (684)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa RefSeq:SWISSPROT-1D:P39062	7.7E-79	16	

456	cg43064068	1464	AGGAGAGGGGTTG AAGGATTGTTGCG /ATTCCTGGCTCGC AGTTCTGCTCCA	G	A	Val (683)	Ile (683)	CONSER VATIVE	Synthetase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COA-ENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.bes;SWISSPROT-ID:P39062	7.40E-65
457	cg2514276	1090	GTGATGGACCCCT TCATAATGCTTAA TTCGGAGCGAGA GATGCGGAAGACC	A	T	Tyr (686)	Phe (686)	CONSER VATIVE	im7	Human Gene SWISSPROT- ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5-R) (MC-2)- HOMO SAPIENS (HUMAN), 325 aa.	7.00E-172
458	cg2423505	964	TICCATCTGAGGT TATAAACCACT/A TATTCAAGGAAAG TGGCCAGATGGC	A	T	Phe (687)	Tyr (687)	CONSER VATIVE	im7	Human Gene Similar to SPTREXB1-ID:Q89609 G PROTEIN-COUPLED RECEPTOR-EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-55
459	cg4333558	344	CAAGACCTAGCTC CCCAAGAGAGAG CTTGCCGCCACA CAAAAGAGGTCCA GC	C	T	Ala (685)	Val (685)	CONSER VATIVE	imceptor	Human Gene Similar to TRIMBLNEWS-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TNAL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89

460	cg43996970	1347	GACAGAGCTGTAC COTGACATTTCIC GIAACACCTTCGGG ATGAAATCAGGCAA	C	G	Gln (689)	CONSER- VATIVE	transcrip-tor factor	Human Gene SPTREMBL- ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12
461	cg2537639	800	GAGGGGGAATCTT ACTACCTCGGGG /CGTTCTCGGGG GTCGGTCAAGAG	G	C	Gly (690)	CONSER- VATIVE	transferase	Human Gene SWISSPROT- ID:Pr642 FUOSYGLYCOPROTEIN ALPHA-N- ACETYLGLACTOSAMINYL TRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUOSYGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT)- HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9 34)

462	cg43935995	1532	AGTGTCCCTGACCG ATGGTCAACCTGIA /GTCACCTCTCCTC TGCTTTCCCTCT	A	G	Ile (69)	CONSER VATIVE	transport	Human Gene SWISSPROT- ID:Q0518 ANTIGEN PEPTIDE TRANSPORTER (APTP) (PEPTIDE TRANSPORTER TAPI) (PEPTIDE TRANSPORTER PSE) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESSING 1)- HOMO SAPIENS (HUMAN), 748 aa.	0	6
463	cg43935986	1424	CCTGAACGCC TTGTAACCTG ATAAGGAGCTG CTGCACTTGGGG T	G	A	Val (692)	CONSER VATIVE	transport	Human Gene SWISSPROT- ID:Q28437 ABC-TRANSPORTER -GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
464	cg43968274	730	GAGCACGAGGAAG CCATGAATGGGC /TCTACTCAGCTA CGCTCACCCAC	C	T	Ala (693)	CONSER VATIVE	UNCLASSIFI ED	Human Gene SWISSPROT- ACC:Q9I44 NEURONAL MUNC18-1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	0	9
465	cg44018398	3368	AGATACCTATA AGCAGTTTAAGC JATGTTAGGAGGA GCTGAATTCAA	G	C	Lys (694)	CONSER VATIVE	UNCLASSIFI ED	Human Gene SWISSPROT- ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) Homo sapiens (Human), 1257 aa.	0	14

466	cg4926796	1825	ACACTGGAAAGCA CAACAGTGTGCA /GTTCTCTCTAGAA AATAATAATTGCA	C	G	Thr (693)	CONSER VATIVE	UNCLASSIFI ED	Human Gene SWISSPROT- ACCQL5046 LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE-TRNA LIGASE) (LYSRS) (KIAA0070) • Homo sapiens (Human), 597 aa.	0	16	
467	cg3055918	1622	AACCGCTGCCTGA CTGAGAAAGCA CTTGATGCTCGTC CACTGCTGAAAC G	C	T	Arg (696)	His	CONSER VATIVE	UNCLASSIFI ED	Human Gene SWISSPROT- ACCP42694 HYPOTHETICAL PROTEIN KIAA0054 • Homo sapiens (Human), 1942 aa.	0	17
468	cg4966985	1381	CATCGAGAACAC TCTCGGTGACTC GAAATGCCCTCA CTGAGAGGCCCTG	C	G	Gln (697)	CONSER VATIVE	UNCLASSIFI ED	Human Gene SWISSPROT- ACCP01019 ANGOTENSINOGEN PRECURSOR • Homo sapiens (Human), 485 aa.	3.90E-257	1 (fq2)	
469	cg43918854	966	CTCAACCCGGTC GGAGACAAGGAA CTCACCATGGCCA TCAGAACAGTCG	A	C	Ile (696)	Leu	CONSER VATIVE	UNCLASSIFI ED	Human Gene SWISSPROT- ACCP20062 TRANSCOBALAMIN II PRECURSOR • Homo sapiens (Human), 427 aa.	3.30E-238	22 (22q11.2)
470	cg3918484	1148	CTGATTCCTCGTT CTCTCTGACTCTG TTGCCACCTGGCCA GGCAAGCTGCTG	C	G	Glu (699)	Gln	CONSER VATIVE	UNCLASSIFI ED	Human Gene SWISSPROT- ACCP063089 ARGINASE 1 (EC 3.5.3.1) LIVER-TYPE ARGINASE • Homo sapiens (Human), 322 aa.	1.30E-171	6 (6q23)

471	cg43942977	1009	ACGGCCTGAGA ACCAAGAGAAGG CTGAGGAAAG AAAGTCCTGATG CC	C	T	Ala (700)	Val (700)	CONSER VATIVE	UNCLASSIFI ED	Human Gene Homologous to SWISSNEW-ACC-012846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148
472	cg43942977	725	GGAIGGTGCGA TCAAGGTTGGAG TTCAGATCTGAA CAGTGGAAAGC G	G	T	Glu (70)	Asp (70)	CONSER VATIVE	UNCLASSIFI ED	Human Gene Homologous to SWISSNEW-ACC-Q15286 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148
473	cg43943361	921	TGGGGTTGGCTTG TTTCAATAASIG CTAACGGGGACT TACAATTCTC	G	C	Glu (702)	Gln (702)	CONSER VATIVE	UNCLASSIFI ED	Human Gene Homologous to SWISSNEW-ACC-P04179 SUPERONIDE DISMUTASE [MD] PRECURSOR (EC 1.15.1.1) - Homo sapiens (Human), 222 aa.	5.70E-124 6 (6e+23.3)
474	cg25236776	1094	GTTACCGACGCCG AGTGGCGCAAGG GATCITTCACCGCC GGGCCGGCCAG C	G	T	Gly (703)	Val (703)	CONSER VATIVE	UNCLASSIFI ED	Human Gene Similar to SWISSNEW-ACC-P01183 VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG, VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-1); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91

475	cg25236776	881	CAGTGCCTCCCGCTG CGGCCCGGGGTC TCAAAGGCCACT CTTGGGCCACGC	G	T	Gly (704)	Val (704)	CONSER ATIVE	UNCLASSIFI ED	Human Gene Similar to SWISSNEW-ACC-G01185 2-COPEPIN PRECURSOR (CONTAINS: ARG- VASCRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPIN); HOMO SAPIENS (HUMAN), 164 aa.	7.20E-91
476	cg38859722	30	GGCCAACCTCTGGT ATGGACACAGAG G/C/TACCTGTGCT GGGGTCATGTCT	G	C	Val (705)	Leu (705)	CONSER ATIVE	UNCLASSIFI ED	Human Gene Similar to REMTREMBL-ACC-G229791 T- CELL RECEPTOR BETA PRECURSOR - HOMO SAPIENS (HUMAN), 145 aa (fragment).	5.70E-75
477	cg11753818	253	GCCCTGAAACCA GGCTCTCTGCTG A/TTCTAAGCTTG TCTCCTAGGAGCA	G	A	Arg (706)	His (706)	CONSER ATIVE	UNCLASSIFI ED	Human Gene Similar to REMTREMBL-ACC-G2104755 T CELL RECEPTOR V-BETA 23 - HOMO SAPIENS (HUMAN), 129 aa (fragment).	1.30E-66
478	cg25236759	519	AGCCACCCAGACC GGAGACTGGCCG /A/TC/TACCTCTG C/CTGAGGCCIA	G	A	Val (707)	Ile (707)	CONSER ATIVE	UNCLASSIFI ED	Human Gene Similar to REMTREMBL-ACC-G331509 T CELL RECEPTOR HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54
479	cg25236759	539	CGGGCGTCACCTC TOTGCTGTGAG/G/ CIGCTATTCATA GACTACAAGCTCA	G	C	Glu (708)	Asp (708)	CONSER ATIVE	UNCLASSIFI ED	Human Gene Similar to REMTREMBL-ACC-G331509 T CELL RECEPTOR HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54

480	cp1902363	368	CAGAACAAAGCA AATGGAATTGAG T/AAGCATCCGGTG GCCCTCTCGAGA	G	T	Glu (709)	Asp (709)	CONSER VATIVE	UNCLASSIFI- ED	Human Gene Similarity to SWISSPROT-ACC-PO1286 SOMATOTROPIN PRECURSOR (GROWTH HORMONE- RELEASING FACTOR) (GRF) (GROWTH HORMONE- RELEASING HORMONE) (GHRH) (SOMATOTROPININ)- Homo sapiens (Human), 108 aa.	2.10E-52	13 (13q41.3)
481	sg33277632	3110	GAACCGGGAGAC ACGTAAATGGCGIA KIGGTCATAAT GCACATGGCTCTG T	A	G	Arg (710)	Gly (710)	NON- CONSER VATIVE	ATTase_associ- ed	Human Gene SWISSPROT- ID:P35670 COPPER- TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE- ASSOCIATED PROTEIN)* Homo Sapiens (Human), 1465 aa.	0	

482	cg43252813	2306	TGTATTCTCTGTAAT GGGGCTGATGAGAC/ TATATAATGATGTT TATGGACCAACAC	C	T	Thr (711)	NON- CONSER- VATIVE	ATPase_associat- ed	Human Gene SWISSPROT- ID:Q04656 COPPER- TRANSPORTING ATPASE 1 (EC 3.6.3.6) (COPPER PUMP 1) (MENCKES DISEASE- ASSOCIATED PROTEIN)- HOMO SAPIENS (HUMAN), 1500 aa;RefSeq:SWISSPROT- ID:Q04656 COPPER- TRANSPORTING ATPASE 1 (EC 3.6.3.6) (COPPER PUMP 1) (MENCKES DISEASE- ASSOCIATED PROTEIN)- HOMO SAPIENS (HUMAN), 1500 aa.	0	X (Xq12)
483	cg43920913	929	GCCCCCTGAGCACT CAGGACCGGGCTC/ TTCGTOCGTGAGT GCCAAGATCCAG	C	T	Pro (712)	NON- CONSER- VATIVE	biotinop- kinase	Human Gene SWISSPROT- ID:Q95166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (POCASE) (PROPYNYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E+288	3 (3q21)
484	cg40310734	267	GGAGGGGGGGTG CTGGCTCTGGAGAC/ GCTCTGGGGGCC CTCCAGGGCTGGGC	C	G	Pro (713)	NON- CONSER- VATIVE	cathepsin D	Human Gene SWISSPROT- ID:Q96514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1BB) (INTEGRIN ALPHAI-B1B) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)

485	cg40310734	3111	CGTGTCCCTCCCTCC CCTATGCGTGTCG GCCCCCTAGGCC TGCCCCGAGGGGA	C	G	Pro (714)	Ala (714)	NON- CONSER- ATIVE	cadherin	Human Gene SWISSPROT- ID108514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GP1IB) (INTERGRIN ALPHAIIB (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
486	cg3956560	777	GGGGTACATGGG CCCCAGTGCACTGTT CTTTGTGATCACT GIGAGCCCTTGA	T	C	Phe (715)	Lys (715)	NON- CONSER- ATIVE	cadherin	Human Gene SWISSPROT- ID14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90- MEL) (LEUKOCYTE- ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E+218	1 (1923)

487	cg43956560	837	GCTGGTACATG GACTGTACTAC/C TCCTGGAACT TCAGCTTCACTC	C	T	Fro (716)	NON- CONSER- ATIVE	cadherin	Human Gene SWISSPROT- ID:P14151 L-SELECTIN PRECURSOR (LYMPHE NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90- MEL) (LEUKOCYTE- ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	I (Iq23)
488	cg42388009	753	TGCAAGAGCAC ACAGAGCGGA AUGGCAGGCA GGCACCTCGAG AC	A	G	Arg (717)	NON- CONSER- ATIVE	cadherin	Human Gene SWISSPROT- ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SIALOPROTEIN) (INTEGRIN- BINDING SIALOPROTEIN)- HOMO SAPIENS (HUMAN), 317 aa.	7.00E-172	4
489	cg43977436	1945	GTTGTGTGAT GGTGGGCTAAC ATGCCAACTGAA GATCTTATTACTGA	C	T	Arg (718)	NON- CONSER- ATIVE	calcium_channel	Human Gene SWISSPROT- ID:P21817 RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE CHANNEL - HOMO SAPIENS (HUMAN), 5032 aa.	0	

490	cg43280376	1130	CGGAAACCTGGTGT CCTACTGCCA GAAAGGTGAA ACTGTTGCCCT	A	G	Gln (719)	NON- CONSER- ATIVE	carboxylase	Human Gene SWISSPROT- ID:F38435 VITAMIN K- DEPENDENT GAMMA- CARBOXYLASE (EC 6.4.-) (GAMMA-GLUTAMYL CARBOXYLASE) - HOMO SAPIENS (HUMAN), 758 aa.	0	2
491	cg42201364	1395	CCAGGGCCTCCAG GTCAGAAGGCCA /CCTCTGGAGAGC CTGGTCTCCAGG G	A	C	Trp (720)	NON- CONSER- ATIVE	collagen	Human Gene SWISSPROT- ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0	6
492	cg42201364	176	GTTGTTACCTGA AGGATACCAAAIC TGGCCACAGGCAT AAAAGGCCCACTA	C	T	Thr (721)	NON- CONSER- ATIVE	collagen	Human Gene SWISSPROT- ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0	6
493	cg40339378	2855	TCCAGGAATACCA GTCCTGCTGTIA GTTCTCTGGAAACA GAGGATAAAAGG	A	G	Ile (722)	NON- CONSER- ATIVE	collagen	Human Gene SWIPEMBL- ID:Q12823 A TYPE IV COLLAGEN - HOMO SAPIENS (HUMAN), 690 aa (fragment).	0	X (X 22)

494	c843063256	606	AGACIGITGTTACC AACAGACCACTCIA /GIGAAGTCAGTG CGATGTAAAGCT T	A	G	Arg (723)	Gly (723)	NON- CONSER VATIVE	complement	Human Gene SWISSPROT- ID: P07358 COMPLEMENT COMPONENT C8 BETA CHAIN (HUMAN), 591 aa; http://www.expasy.org/sprot/ID:P07358	0	1 (1p32)
495	c844032748	414	CTCAGCTCACAA A CTTGTCIAAGGIA CJAAGCACAGTGCG GACAGGATTCCA	A	C	Lys (724)	Gln (724)	NON- CONSER VATIVE	complement	Human Gene SWISSPROT- ID: P07357 COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR HOMO SAPIENS (HUMAN), 584 aa.	0	1 (1p32)
496	c843049885	333	CAGTTGGGGAC A AGCCATGACTGTA /CTGCCTCTGTAGC CTTCAACATGC	A	C	Glu (725)	Ala (725)	NON- CONSER VATIVE	complement	Human Gene TREMBLNEW- ID: G36348 COMPLEMENT C6- HOMO SAPIENS, 941 aa.	0	5 (5p13)
497	c82164442	1347	CCAGGCTCTCCA T GGATCTCATCACTT CTCGGCCCGAGG CCTCAAGAAACCC	T	C	Leu (726)	Pro (726)	NON- CONSER VATIVE	csf	Human Gene SWISSPROT- ID: P095603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCFD), HOMO SAPIENS (HUMAN), 554 aa.	5.00E-304	1 (1p31)

498	cg2753430	279	CCAGGCTCCATG ACCAAGACAAGC TICCTGAAACCA AGCTGGTTAACT G	C	T	Pro	Ser (727)	NON- CONSER- VATIVE	csf	Human Gene Similar to SWISSNEV-ID: P08700 INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOENTIAL COLONY-STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CRLL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCFP) - HOMO SAPIENS (HUMAN), L52 SwissProt ID:P08700 INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOENTIAL COLONY-STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CRLL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCFP) - HOMO SAPIENS (HUMAN), L52 aa.	1.10E-77	5
499	cg43923204	1651	TCCACGTAGAACG GGAAGCCCGAGTT AGGGAGATGIAAC GCATTGATGGAA GG	A	G	Tyr	His (728)	NON- CONSER- VATIVE	cyclochrome	Human Gene Similar to SWISSPROT-ID: P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

500	cg4017721	174	TGGTAGGAGACCG AACTGGGGCGGTG TGAGGGTGGGCC GAGTTGAGATAGG A	G	T	Pro (729)	Gln (729)	NON- CONSER- ATIVE	cytochrome oxidase	Human Gene Similar to CYTOCHROME OXIDASE SUBUNIT VIA HEART, ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME-C A(3)) (CYTOCHROME-AA(3))- HOMO SAPIENS (HUMAN), 97 aa.	2.40E-52	22
501	cg4162624	279	OCTGGTTTGCTCC AGGAGGCCAG/A CAGTCAGCTACT GCCCTACATCA	A	C	Lys (730)	Gln (730)	NON- CONSER- ATIVE	deaminase	Human Gene Similar to SWISSPROT-ID:P32320 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) • HOMO SAPIENS (HUMAN), 146 aa. alt:swissprot:TRENBLNEW- ID:1E1ZB8801 CYTIDINE DEAMINASE (EC 3.5.4.5)- HOMO SAPIENS (HUMAN), 146 aa.	8.80E-78	1 (p36.2)
502	cg43057018	1618	AAGCATCGAACAA ATCCATCTTITV GIGAAGATGCAG GAGCAATTGCAA T	T	G	End	Gly (731)	NON- CONSER- ATIVE	dehydrogenase	Human Gene SWISSPROT- ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) • HOMO SAPIENS (HUMAN), 391 aa. alt:swissprot:TDP08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1)- HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)

503	cg42837709	464	CCGCACCAACCGC GACATCATGAGIA GCCCTGAAGAG AAGGGCTCAAGG G	A	G	Thr (732)	Ala (732)	NON- CONSER- ATIVE	dna_ma_bind	Human Gene Similar to TRIMBLE-NEW-ID:Q9J312 DNA BINDING PROTEIN MEF2 (CLONE XMREF2A1) XENOPUS LAEVIS, 516 aa.	3.90E-86	1
504	cg43327954	2205	TCCAGACGGGGT AGAGACTAACAI CAACGGGGAGC GAAAGCTCGCAA CC	C	A	Lys (733)	Asn (733)	NON- CONSER- ATIVE	dna_ma_bind	Human Gene Similar to SPTRIMBLE-ID:Q61491 DNA- BINDING PROTEIN - MUS MUSCULLUS (MOUSE), 546 aa.	5.50E-57	1
505	cg43971258	707	TGTGAGATGA CAAGTCGGAGIC TTAGCTCGCTGT CTGGATGGAGG	C	T	Ala (734)	Thr (734)	NON- CONSER- ATIVE	dna_ma_bind_in rib	Human Gene Similar to SWISSPROT-SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HHL (R2)) (HELIX- LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa/pols-SWISSPROT- ID:Q02535 DNA BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HHL (R2)) (HELIX-LOOP- HELIX PROTEIN HEIR-1)- HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (p46.13)

506	cg41554010	1253	AGCTGGACCAACA GCAGGAAAGCAGC GTTCAAGGAGAGC AGCAGGAGGAGGT GC	G	T	Gln	His (735)	NON- CONSER- ATIVE	epha	Human Gene SWISSPROT- ID: P06727 APOLIPOPROTEIN A- IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa. Incls: SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)* HOMO SAPIENS (HUMAN), 396 aa.	1.80E-203 (11q23)	11
507	cg43957743	1063	GTTGGCATACCTG GATATTAAATCT]CA GTTGAGATAA AAGACAGCCACT	C	T	Gly	Glu (736)	NON- CONSER- ATIVE	esterase	Human Gene SWISSPROT- ID: Q15166 SERUM PARAOXONASE/ARYLESTERA- SE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM) ARYLDIARYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment). Incls: SWISSPROT- ID: Q15166 SERUM PARAOXONASE/ARYLESTERA- SE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM) ARYLDIARYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment).	1.90E-178	

508	0845957743	1079	TATTTAATCAGT GGAGATAAAGA/ CICAGGCCACTAGG AAGTATATCATA	A	C	Ser (737)	NON- CONSER- VATIVE	cstterase	Human Gene SWISSPROT- PARAOXONASE/ARYLESTERA- SE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIARYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3)- HOMO SAPIENS (HUMAN), 341 aa (Fragment); bndl: SWISSPROT- IDQ15166 SERUM PARAOXONASE/ARYLESTERA- SE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIARYLPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3)- HOMO SAPIENS (HUMAN), 341 aa (Fragment).	1.90E-178	
509	0843248101	812	AAGTGAATTAT CTTGCATATGACIA /GJAGGAAGGAAA CTCTATGCAAGAA A	A	G	Lys (738)	NON- CONSER- VATIVE	fgf	Human Gene Homologous to SWISSPROT-ID:P21781 KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR-7) (FGF-7) (HBGF-7)- HOMO SAPIENS (HUMAN), 194 aa.	9.30E-106	15 (1sq15)

510	cg43969014	332	GATGAGCTCCCA ACCACGTATTTCI AATGCCCTTTGAT CCAGACCCAGATG	C	A	Arg (739)	Ile (739)	NON- CONSER- VATIVE	glucuronidase	Human Gene Similar to SWISSPROT-ID:P08236 BETA- GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	7.40E-80	5
511	cg43286488	387	CACCGAAAGATG CCCACATCAGCTG TGGAACCTGCCA AGGCCTCTCTTG	G	C	Pro (740)	Arg (740)	NON- CONSER- VATIVE	glycoprotein	Human Gene SWISSNEW- ID:P40967 MELANOCTE PROTEIN PNL 17 PRECURSOR (MELANOCTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA- ASSOCIATED ME20 ANTIGEN) (ME20/M/ME20S) (ME20- M/ME20-S) (95 KD) MELANOCTE-SPECIFIC SECRETED GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 661 aa. (PESWISSPROT ID:P40967 MELANOCTE PROTEIN PNL 17 PRECURSOR (MELANOCTE LINEAGE- SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20/M) (ME20-M / ME20-S) (95 KD) MELANOCTE-SPECIFIC SECRETED GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 661 aa.	0	12

512	cg44004239	663	TTCGCCAGGGT CACAGACTGATTA GIACCCCACAGAGGT CAGGGTCCTGCT	A	G	Tyr (741)	His (741)	NON- CONSER- VATIVE	glycoprotein	Human Gene SWISSPROT- ID:Q12889 OVDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVDUCTAL GLYCOPROTEIN) (OVDUCTIN) (ESTROGEN- DEPENDENT OVDUCT PROTEIN)- HOMO SAPIENS (HUMAN), 678 aa.	0
513	cg44004239	672	GGGTCAACAGACT GATAACCAACAGA QIGGTCAAGGTCT TCCTTCAGGGTC	A	G	Ser (742)	Pro (742)	NON- CONSER- VATIVE	glycoprotein	Human Gene SWISSPROT- ID:Q12889 OVDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVDUCTAL GLYCOPROTEIN) (OVDUCTIN) (ESTROGEN- DEPENDENT OVDUCT PROTEIN)- HOMO SAPIENS (HUMAN), 678 aa.	0
514	cg44004239	773	CCTATGACCCACA GAAGTCATGTCIA QGTTCGCCAGTG ATCTAGTCCTC	A	G	Met (743)	Thr (743)	NON- CONSER- VATIVE	glycoprotein	Human Gene SWISSPROT- ID:Q12889 OVDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVDUCTAL GLYCOPROTEIN) (OVDUCTIN) (ESTROGEN- DEPENDENT OVDUCT PROTEIN)- HOMO SAPIENS (HUMAN), 678 aa.	0

515	cg43932434	1504	ATATGTTCTACT GGGAGGTGTTG/ TIAATGAGGAATG ACACCCCTGTGTT	G	T	Ser (744)	NON- CONSER- ATIVE	glycoprotein	Human Gene SWISSPROT- ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN 1) (PGP-1) (HUCH-1) (EXTRACELLULAR MATRIX RECEPTOR-II) (ECMR-II) (GP90)	1.80E-195 11 (1 pter)
516	cg40915005	622	AAGGAGCTCTCT CCCTCCATGTCAGC/ TCTGGATCGATC CTTTACACCAT	C	T	Thr (745)	NON- CONSER- ATIVE	glycoprotein	Human Gene SWISSNEW- ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/ELU-6) (HTAI THYMOCYTE ANTIGEN) -HOMO SAPIENS (HUMAN), 327 aa.lengthSWISSPROT-ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/ELU-6) (HTAI THYMOCYTE ANTIGEN) -HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183 1 (1g21)

517	cg40915005	737	ATTCAGCACACAT CGTTTCCCTGTGCG CICCCGTCGCAAG GGAAACTCGACA	G	C	Tyr (746)	NON- CONSER- ATIVE	glycoprotein	Human Gene SWISS-PROT ID: P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTLA THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa. IEds/SWISS-PROT:ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTLA THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183	1 (q21)
518	cg36834323	1529	GTGCTCCTGATGCC TCGTGAAGCTAA/ GTTGTAAGCTAAAG TIAATGCGCATCT	A	G	Tyr (747)	NON- CONSER- ATIVE	glycoprotein	Human Gene Similar to SWISS-PROT:ID:P28159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
519	cg36834323	329	AAATGCTGGAAAG ATATGATGAAIA CGCTCTTGATGG AAAAGCAAAAAA	A	C	Lys (748)	NON- CONSER- ATIVE	glycoprotein	Human Gene Similar to SWISS-PROT:ID:P28159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	

520	cg36834323	463	AAGCTTGAGCTT GCAAGGAGAAC AATGTGAGAAAC AAAGGGTGCTT CC	A	C	Ser (749)	Arg (749)	NON- CONSER- VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
521	cg44019290	1697	GCGGATAAAGTAGA GGACCTCATGTTT GIGTATTGCGCTG GAAGTTGTCGG	T	G	Asn (750)	His (750)	NON- CONSER- VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:PP04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.30E-30	11
522	cg42336656	1665	CCTAGACATACA TATACTACCTT[A/ G]GAGGTCAAG[T/A C]TTGCCCCACA	A	G	Arg (751)	Arg (751)	NON- CONSER- VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q05910 CELL SURFACE ANTIGEN MS2 PRECURSOR (EC 3.4.24.-) (MACROPHAGE CYSTEINE- RICHE GLYCOPROTEIN) (CD156 ANTIGEN) - MUS MUSCULUS (MOUSE), 826 aa.	9.40E-58	
523	cg42730678	980	GGAGCGAGCTGG ATCCAGTCGGCGG TGGGGTTGTTG GGTCAAGTCTG	G	T	Ala (752)	Asn (752)	NON- CONSER- VATIVE	homeobox	Human Gene SWISSPROT- ID:PP8356 HOMEBOX PROTEIN HOX-D9 (HOXA-4C) (HOXA-5.2) - HOMO SAPIENS (HUMAN), 342 aa.	2.60E-188	2

524	cg42714160	769	GCCCTGTGGCTGAG CGGAGAGCAGA TGGCAAGATATGG TTCAGAAACGAC GC	T	G	Ile (753)	Ser (753)	NON- CONSER- ATIVE	homeobox	Human Gene Homologous to HOMEOBOX PROTEIN HOX-B6 (HOX-3B) (HOX-2.2) (HUMAN), 224 aa.	1.10E-123
525	cg42359655	3297	CCTGGCACCATAT AGGATAGCCACIA /GJCCGTCATCAA GCCCATGGCAGAG T	A	G	Thr (754)	Ala (754)	NON- CONSER- ATIVE	hydrolase	Human Gene SWISSPROT: ID:PP9648 LACTASE- PHOSPHORYLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYL CERAMIDEASE)- HOMO SAPIENS (HUMAN), 1927 aa.	0 2 (2421)
526	cg43925670	2172	GTCGAGGGTGCGAG GTGAAGTAGAACAT /QGACTTCCTCTT CCTCTTCGAT	C	G	Asp (755)	His (755)	NON- CONSER- ATIVE	interferon	Human Gene SWISSPROT: ID:Q16666 GAMMA- INTERFERON-INDUCIBLE PROTEIN IFN-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa Swiss-Prot:EMBL-DB:Q16666 IFN-16 INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0 1

527	cg43050990	1083	TGCUTCATCAAA ATGAGCAAGC CTTGCCATGTTAC CGACACGGAAAA A	C	T	Pro (756)	Lys (756)	NON- CONSER- ATIVE	kinase	Human Gene SWISSPROT®- ID:Q4759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPYC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0	10
528	cg43969763	2663	CAAAAGCAGAAA GTTCITTGAAAGC TTTGCAGAGTGC ACTTGGAACTAA	G	T	Lys (757)	Asn (757)	NON- CONSER- ATIVE	kinase	Human Gene SWISSPROT®- ID:Q13677 SERINE/TYROSINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-)(HPF86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0	21 (21q22.1)
529	cg43932396	1226	AGTCACGGCGC CTTGGCCGTC TGTCTGGCGAGT AGGAGAACTGGGG G	C	T	Gly (758)	Ser (758)	NON- CONSER- ATIVE	kinase	Human Gene SWISSPROT®- ID:P31749 RAC-ALPHA SERINE/TYROSINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C- AKT) - HOMO SAPIENS (HUMAN), 480 aa.	14	14 (14q32.3)
530	cg43917871	1429	GGCACTGAAGAAA TCCTGACATCAITV CIATGGGGCTCT GAAGGGGGTACTG	T	C	Met (759)	Val (759)	NON- CONSER- ATIVE	kinase	Human Gene SWISSPROT®- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
531	cg43917871	1621	GGGCTGACAAGGT GCTGATTTACATV GTTGGACAAAGC GTTCCTATGCTT	T	G	Ser (760)	Arg (760)	NON- CONSER- ATIVE	kinase	Human Gene SWISSPROT®- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)

532	cg43917871	1713	TCCAATGTTGTAIT TGTCATAATAATGTC ICATATAAAATCTC TGTCCCCCAGAAC	T	C	Asp (761)	Gly (761)	NON- CONSER- ATIVE	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215 (20p13)	11 (20p13)
533	cg43917871	2096	TGTAATAATGGAAAT ATCATAGTCCTGTTC GIAACGTCGGTAC AATTCGTTGAAGT	T	G	Leu	Phe (762)	NON- CONSER- ATIVE	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215 (20p13)	11 (20p13)
534	cg43922345	1107	TCGGCTAGGGAGC CTCCATCCCTCACAA CJCCCTTATACACA TCCGGCTGGCATG	A	C	Thr (763)	Pro (763)	NON- CONSER- ATIVE	kinasereceptor	Human Gene SWISSPROT- ID:P30330 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. swissprot (HUMAN), 887 aa. TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0 (19q13.1)	19 (19q13.1)

535	284332345	2116	TTCCTCTATTC CCGCTGGGGAA GCCAACCAAGTCA CCTGCCCACTCAG	A	G	Asp (764)	Gly (764)	NON- CONSER- ATIVE	kinaserceptor	Human Gene SWISSPROT- ID:P0530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE - HOMO SAPIENS (HUMAN), 887 aa [Pdb:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa]	0	19 (18q13.1)

536	cg43958558	863	TCCGGATTAAGCT CCAAGGTGCTCAG TGTGTTAGGCCCT GGAGGTGCCGTGTC C	G	T	Pro (765)	His (765)	NON- CONSER- ATIVE	laminin	Human Gene Homologous to SWISSNEW-1DPI7931 GALECTIN-3 (GALACTOSE- SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) -HOMO SAPENS (HUMAN), 249 aa.Idols:SWISSPROT-IDP7931 GALECTIN-3 (GALACTOSE- SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) -HOMO SAPENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)
537	cg4396144	718	AAGCTTGTCATGC CITACAGCACTGC AAGCACAGACTGC CCAGGCCAAATGG A	C	A	Ala (766)	Glu (766)	NON- CONSER- ATIVE	MHC	Human Gene Homologous to SWISSPROT-IDP8068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPENS (HUMAN), 263 aa.	9.10E-147	6 (6p21.3)

538	cg3966144	823	ACTTACACCTGGTGT GGTAGAACCATG CITGGGGCTCTGGA GCCCATCTTCGG	T	C	Ile (767)	Thr (767)	NON- CONSER- ATIVE	MHC	Human Gene Homologous to SWISSPROT-ID:P28063 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147 (6p21.3)	6
539	cg42686658	907	GGCCTGGTGGGCT TCCTCTGGGAGC/ TJGTCCTCACAT CATGGGCACAT	C	T	Thr (768)	Le (768)	NON- CONSER- ATIVE	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, D2 ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134 (6p21.3)	6
540	cg3837533	1044	CTAGGCCAGAGC GTTGCTCTGTC/ GICATGAGGACAC AGTCAGGCTCTGA	C	G	Pro (769)	Ala (769)	NON- CONSER- ATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.30E-113 (19)	19
541	cg3837533	424	AGCCCGCCGGGC CCACCGGTGCTA GJAGGAGAAAC GTGACCTTGCTG	A	G	Thr (770)	Ala (770)	NON- CONSER- ATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.30E-113 (19)	19
542	cg32481172	340	CCGGCTGTGCTCA GGGGTGGGGTGA GJGGGATAACAG GAGGGCTGTGG A	A	G	Thr (771)	Ala (771)	NON- CONSER- ATIVE	misc_channel	Human Gene Similar to SPTREMBL-ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CANONRABEDITIS ELEGANS, 461 aa.	2.30E-71 (1)	1

543	cg3100465	238	GAAATGCCCTCC TCAGACATGAGTGT TGAAAGTTATC AGAAATGGTCCG C	G	T	Leu (772)	NON- CONSER- ATIVE	miss_channel	Human Gene Similar to SPTREMBL-ID: P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	6.10E-70 (8p11.2)
544	cg3100465	240	AGATGCCCTCCTC AGACATAGCTG A A/CAGATTATCA GAATGGTCCG CC	A	C	Lys (773)	NON- CONSER- ATIVE	miss_channel	Human Gene Similar to SPTREMBL-ID: P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	6.10E-70 (8p11.2)
545	cg43249083	1067	GCCCTGGCTTCC ACTACGTTGCTCA T TGCGCTGGAGG GCTCAAGCTT T	A	T	His (774)	NON- CONSER- ATIVE	nuc_recept	Human Gene SWISSPROT- ID:P20592 V-ERBB-1 RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0 (17q11.2)
546	cg44928796	68	AGCGGAGGTC GGACAAAGCC G GCAAGGAGGA GGGACAGAGGA AA	G	C	Gln (775)	NON- CONSER- ATIVE	nuc_recept	Human Gene SWISSPROT- ID:P0275 ANDROGEN RECEPTOR - HOMO SAPIENS (HUMAN), 919 aa. (Ref:SWISSPROT-ID:P10275 ANDROGEN RECEPTOR - HOMO SAPIENS (HUMAN), 919 aa.)	0 X(Xq11)
547	cg43323772	91	GTGCCGGAGTGA GGCATGAGCTGG T TTCCTGTTCTGG CCGACAGAGTCGC	C	T	Leu (776)	NON- CONSER- ATIVE	nuclease	Human Gene TREMBL NEW- ID: G2935442 RIBONUCLEASE H1 - HOMO SAPIENS (HUMAN), 286 aa. (Ref: TREMBL NEW- ID: G2935442 RIBONUCLEASE H1 - HOMO SAPIENS (HUMAN), 286 aa.)	1.40E-157

548	9842732993	809	GGCTATATACTACA ATGGGAGATGTG /TTGAAQCCAAA CCAAAATGGCCA A	G	T	Cys (777)	Phe (777)	NON- CONSER- ATIVE	oncogene	Human Gene Homologous to SPTREMBL-ID:Q13692 BCRABL FUSION PROTEIN - HOMO SAPIENS (HUMAN), 284 aa (fragment).	6.00E-150	
549	cg42904626	155	AATAAACHTGTC GTAGTGGAGCTG /JGIGGGTAGGC AAGAGTGCTTG C	G	T	Gly (778)	Cys (778)	NON- CONSER- ATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:POU118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12
550	cg42904626	304	TGGATATTCTCGAC ACAGCAGTCATA/ CIGAGGAGTCACT GAATAGGGACC	A	C	Gln (779)	His (779)	NON- CONSER- ATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:POU118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12
551	9842691989	706	CIGTCAGGATC/C CTCATCTGACIA/T JGTTCTCTGTG CCAAATTTGTTG	A	T	Cys (780)	Ser (780)	NON- CONSER- ATIVE	peroxidase	Human Gene Homologous to SWISSPROT-ID:PI8283 GLUTATHIONE PEROXIDASE - GASTROINTESTINAL (EC 1.11.19.9 (GSHPx-GD) (GLUTATHIONE FEROXIDASE - RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.50E-101	14 (14q24.1)

552	cg43917453	4096	AGGTCTCGGGA GCTGGTCCGGIA (GCCCGGGAGCT AEGTCAGCGAGA C	A	G	Ser (781)	Pro (781)	NON- CONSER- VATIVE	phosphatase	Human Gene TREMBL NEW- ID:G2262075 IAR/RECEPTOR- LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), (015 aa).	0	7
553	cg43947363	3168	CTGGCGCACTACT CGGACCTGCTC/C/ TCTCTGGGGGCGCT GGGGCTATGAG	C	T	Gly (782)	Glu (782)	NON- CONSER- VATIVE	phosphatase	Human Gene SWISSPROT- ID:DP2469 PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R- PTP-EPSILON) -HOMO SAPIENS (HUMAN), 700 aa.	0	
554	cg43928335	3187	GACAAGGAACGG AAATTGCTGTC[A/ GTTTCCTCTTAA CAGCATTTGAGC	A	G	Ile (783)	Thr (783)	NON- CONSER- VATIVE	phosphatase	Human Gene SWISSPROT- ID:DP4613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS CROFA (PIG), 602 aa (fragment).	3.20E-302	11 (11q22)
555	cg43996195	1330	CITCGGGAAAGT TGGGGATTAC/C/ TGTAGTCAAAGAT CTGGGCTGAGT	C	T	Gly (784)	Ser (784)	NON- CONSER- VATIVE	phosphorylase	Human Gene SWISSPROT- ID:DP0461 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE (PNP)) -HOMO SAPIENS (HUMAN), 289 aa.	2.40E-155	

536	cg44022214	3340	AGGUCCTCCCGA ATGGGATGGCQA GJAGGTGCACTAT CATCATCCCCAGAG G	A	G	Trp (785)	Arg (785)	NON- CONSER- ATIVE	polymerase	Human Gene SWISSPROT- ID: P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. Isc-SWISSPROT-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)
537	cg43958858	1593	CITCAGACCATGTC CITCGGATGCAC/C GIGTTACAGAGAC CTGGGGAGCAGGA	C	C	Gly (786)	Arg (786)	NON- CONSER- ATIVE	polymerase	Human Gene SWISSPROT- ID: P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA, HOLONYZME-ASSOCIATED PROTEIN PI) (RLF BETA SUBUNIT) (P102 PROTEIN)- HOMO SAPIENS (HUMAN), 808 aa. Isc-SWISSPROT-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA, HOLONYZME-ASSOCIATED PROTEIN PI) (RLF BETA SUBUNIT) (P102 PROTEIN)- HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)

558	cg42345468	641	CGCTTGGAGCCGC AEGTGGCACCCIA TGCGCAGTC CAACACACTCTG	A	T	Gln (787)	Leu (787)	NON- CONSER- ATIVE	potassium Chan nel	Human Gene SWISSPROT- ID:P22460 VOLTA GE-GATED POTASSIUM CHANNEL PROTEIN KV.1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
559	cg42345468	868	GGGGGAGGAGGCC ATGGAGGCCCTTC TGCGGAAGGAGAG GGCTTCATTAAAG A	C	G	Arg (788)	Gly (788)	NON- CONSER- ATIVE	potassium Chan nel	Human Gene SWISSPROT- ID:P22460 VOLTA GE-GATED POTASSIUM CHANNEL PROTEIN KV.1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
560	cg42345468	910	CATTAAAGAAGAG GAGAAAGCCCTGC TGCGCGCAAGAG TTCAAGGCCAGG T	C	G	Pro (789)	Ala (789)	NON- CONSER- ATIVE	potassium Chan nel	Human Gene SWISSPROT- ID:P22460 VOLTA GE-GATED POTASSIUM CHANNEL PROTEIN KV.1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
561	cg43154190	898	TGGAGGGGAGCT CATTTGATGAAAG CIACTGAAAGGTG ACCAAACATTCA G	G	C	Asp (790)	His (790)	NON- CONSER- ATIVE	protease	Human Gene Similar to SWISSPROT-ID:P50280 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN), RATTUS NORVEGICUS (RAT), 267 aa.	2.40E-59	11 (11q22)

562	cg43154190	923	GATGAAAGGGGA CCACCAATTCAIG CIAAGACTACA TACATCGTGCG	G	C	Arg (791)	Thr (791)	NON- CONSER- VATIVE	protease	Human Gene Similar to MATTRYL/SIN PRECURSOR (EC 3.4.2.23) (PLA2R PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7)(MATRIN). RATITUS NORVEGicus (RAT), 267 aa.	2.40E-59 (1.1q22)	11
563	cg43227549	694	ATTCACGATTCGG GTTTACGTCAGGT CTTAACCTAGGCC CTTTCCTAAC	G	T	Gly (792)	Cys (792)	NON- CONSER- VATIVE	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NADPH DEHYDROGENASE (QUINONE) 2 (EC 1.6.9.2) (QUINONE REDUCTASE) (DT- DIAPHRASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) • HOMO SAPIENS (HUMAN), 231 aa.	1.60E-14 (6pter)	6
564	cg43225541	1081	CGCTGCCTCC GAAGGGTCCTC TCTCTACCGTT CGCTCCGGAG	C	T	Gly (793)	Glu (793)	NON- CONSER- VATIVE	synthase	Human Gene TREMBLNEW- ID:GT2725625 ACETOLACTATE SYNTHASE, HOMO SAPIENS (HUMAN), 632 aa.	0	19

565	cg33064068	1474	GTTAGGGCATTTG TGGCTCTGGACCTC/ TGGCAATTTCCTGTC CCATGACCCAGAA	C	T	Ser (794)	Leu (794)	NON- CONSER- ATIVE	synthase	Human Gene Similar to ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) -BACILLUS SUBTILIS, 572 aa [ipr] SWISSPROT ID:P39062	7.40E-55
566	cg33064068	1617	GACTGTACAGGG AAAATICAAGGA AAGCAAGCTTCA GACAAGGA A	G	A	Ala (795)	Thr (795)	NON- CONSER- ATIVE	synthase	Human Gene Similar to ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) -BACILLUS SUBTILIS, 572 aa [ipr] SWISSPROT ID:P39062	7.40E-55

567	cg36988276	1119	GCAAGAAGTTGAT TATTAACGTAGIA /GCTAGGGTCAG AGATCCCTCTGGC	A	G	Thr (796)	Ala (796)	NON- CONSER- VATIVE	tm7	Human Gene SWISSPROT- ID:P23945 FOLLICLE- STIMULATING HORMONE RECEPTOR PRECURSOR (FSH- R) (FOLLITROPIN RECEPTOR)- HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
568	cg36988276	335	AAGGCCAACACACC TGCTCTACATCA/A/ CICCTGAGGCCT CCAGAACCTTC	A	C	Asn (797)	Thr (797)	NON- CONSER- VATIVE	tm7	Human Gene SWISSPROT- ID:P23945 FOLLICLE- STIMULATING HORMONE RECEPTOR PRECURSOR (FSH- R) (FOLLITROPIN RECEPTOR)- HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
569	cg32296648	1475	GAATGCTGAGA ATCCAGTGTCTC/T TGCGAGAAAGACT CTTCCAAACATGC	C	T	Arg (796)	Cys (796)	NON- CONSER- VATIVE	tm7	Human Gene SWISSPROT- ID:P5548 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA-1A-ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR)- HOMO SAPIENS (HUMAN), 466 aa.	1.60E-252	8 (8p21)
570	cg224739	1590	TCTCTGAGAA GATCACCACATC /GJACACAAACGG TCAGCACCAACC T	C	G	Ile (799)	Met (799)	NON- CONSER- VATIVE	tm7	Human Gene SWISSPROT- ID:P21728 D1A DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 446 aa.	8.30E-240	5 (5q5.1)

571	cg2320320	394	AGTGTCTGGATGA TCCTTGTCGCAc/ TTCGATCCGTT CACAAATGGCCTT	C	T	Thr (800)	NON- CONSER- ATIVE	tm7	Human Gene SWISSPROT- ID: P4001 GREEN-SENSITIVE OPsin (GREEN CONE PHOTORECEPTOR PIGMENT) -HOMO SAPIENS (HUMAN), 364 aa.	8.50E-199
572	cg43264978	519	CACTCTCCATCA ACCTCTCACAG JGCATTTCCTCTC ACGTGATGAG	A	G	Ser (801)	NON- CONSER- ATIVE	tm7	Human Gene TREMBLYNEW- ID: G2736282 G PROTEIN- COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 352 aa.	1.40E-196
573	cg3033708	285	TCTTGTGGACAT CTGCTCTCCCTC CACCACTGCC AAGATGTGCC	T	C	Phe (802)	NON- CONSER- ATIVE	tm7	Human Gene TREMBLYNEW- ID: E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.30E-160
574	cg3841806	68	GGCCTGAGGCA ACACCGGGCACT C/CACAGCCCTC CATGCCAGCTGG	T	C	Ile (803)	NON- CONSER- ATIVE	tm7	Human Gene Similar to SWISSPROT-ID: P10975 TACHYKININ-LIKE PEPTIDES RECEPTOR 90D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-57
575	cg43336100	688	TGGAAGGGTGTCA CCAGTGAAGACAA /TTGAGGTGACT CTTTAGTCCTG	A	T	Met (804)	NON- CONSER- ATIVE	tuf	Human Gene SWISSPROT- ID: P26022 PENTAXIN- RELATED PROTEIN PTX3 PRECURSOR (TUMOR, NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) -HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207 3 (3425)

576	cg43335562	234	GAGGCCGGGAG CCAGGCCCTGGCCT /CICCGGATGCCCA AGACCCCTTGTCCT	T	C	Leu (805)	NON- CONSER- ATIVE	transfector	Human Gene Similar to TREMBL/INFN-1/D-G263845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
577	cg43140548	2857	ACTCGACGCGGA TCCTGAGCTGTAA GAGAGGTAGGA AGGCTTGACACA G	A	G	Tyr (806)	NON- CONSER- ATIVE	transfector	Human Gene SP1/TREMBL- ID:Q14872 METAL- REGULATORY TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 753 aa.	0	1
578	cg43011261	1285	CATTGACAGGGAG GCCCTCTCACCC/C TTCCTCATGGCA AGAAAAGACGCC	C	T	Leu (807)	NON- CONSER- ATIVE	transfector	Human Gene SWISSPROT- ID:P35269 TRANSCRIPTION INITIATION FACTOR III, ALPHA SUBUNIT (TFIIF- ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa.	4.30E-275	19 (19p13.3)
579	cg43988970	1346	TGACAGAGCGTA CCGTGACATTTTC GTCAGGACCTTCGG GATGAAATCGCA	C	G	Phe (808)	NON- CONSER- ATIVE	transfector	Human Gene SP1/TREMBL- ID:Q02729 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12

580	c82337639	464	CACTATAGTCCTT C CACCGACCAGC/C/ TGGCGCGGTGCC CCGGTGACCTG	C	T	Pro (809)	Lau (809)	NON- CONSER- VATIVE	transferrase	Human Gene SWISSPROT- ID:P1642 FUCOSYLGlycoprotein ALPHA-N- ACETYL GALACTOSAMINYL T RANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE)/ FUCOSYLGlycoprotein 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAcAT)* HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192 9 (9q34)

581	cg237639	523	TCCGCAAGCTTCAC GTCGTGGAGGTGIC CGCTGCAGGACG T	C	G	Arg (810)	Chy (810)	NON- CONSER- ATIVE	transferease	Human Gene SWISSPROT- ID:P1642 FUCOSYLYCOPROTEIN ALPHA-N- ACETYLGLACTOSEAMINYL T RANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLYCOPROTEIN 3- ALPHA- GALACTOSYLYL TRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAcAT) HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192 9 (943)
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582	cg2337639	643	GGTGTGGGTGAC GTGGACATGGAGT (ATTCGGGACAC GTGGCGTGAGA T	A	Phe (811)	Ile (811)	NON- CONSER- ATIVE	transfase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGlycoprotein ACETYL GALACTOSAMINYL T TRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE)/ FUCOSYLGlycoprotein 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT)- HOMO SAPIENS (HUMAN), 354 aa.	6.30E-192 9 (934)

583	cg2577639	700	TCCGCTGTTCGGCA G CCCTGACCCCGI AIGCTTCTAACGAA GCAGCGGGAGGC	A	Gly (812)	Ser (812)	NON- CONSER- VATIVE	transferease	Human Gene SWISSPROT- ID:P16442 FUCOSYGLYCOPROTEIN ALPHA-N- ACETYLGALACTOSAMINYLT RANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE (A TRANSFERASE) / FUCOSYGLYCOPROTEIN 3- ALPHA- GALACTOSYLTTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.30E-192	9 (934)
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584	cg2337639	793	CAGGAGCGGGC GATTCTACTAC/C AATGGGGGGTCT TCGGGGGTCCGT	C	A	Leu (813)	Mat (813)	NON- CONSER- VATIVE	transfase	Human Gene SWISSPROT- ID:P16442 FUcosylglycoprotein alpha-N- Acetylglucosaminyl transferase (EC 2.4.1.40) (Histo-blood group A transferase) (A transferase)/ Fucoxylglycoprotein 3 alpha- galactosyltransferase (EC 2.4.1.37) (Histo-blood group B transferase) (B transferase) (N-acat) Homo sapiens (Human), 354 aa.	6.50E-192	9 (9q34)

585	cg2437639	826	GTTCCTGGGGGG TCGTTCAAATAGG /ATGCCAGCGCTC ACCAAGGCCCTGCC A	G	A	Met (814)	Val (814)	NON- CONSER- ATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLYLGLYCOPROTEIN ALPHA-N- ACETYL GALACTOSAMINYLT RANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE)/ FUCOSYLYLGLYCOPROTEIN 3- ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) HOMO SAPIENS (HUMAN), 354 aa.	6,50E-192	9 (9x34)
586	cg42742340	3249	CACATGTTGG AGCTGACCCAGGC /ATGACCTTCTGG GCTCAGGTGGCG G	C	A	Asp (815)	Ala	NON- CONSER- ATIVE	transport	Human Gene SWISSPROT- ID:Q04671 P PROTEIN (MELANOCT-TE-SPECIFIC TRANSPORTER PROTEIN)* HOMO SAPIENS (HUMAN), 838 aa.	0	15
587	cg41633463	427	GTCGTAAAGATT CCACAAGGAGAC /GCTGAAAGCCTC ACCAAGGAAGAGC C	C	G	Ile	Met (816)	NON- CONSER- ATIVE	transport	Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa.	0	3 (3p25)

588	cg46351913	1165	CAA/GTTACCAAC AACTGTACAGGG /CAGCGATTC ACCACCTCATCA A	G	C	Asp (817)	His (818)	NON- CONSER- ATIVE	transport	Human Gene SWISSPROT- ID:Q01959 SODIUM- DEPENDENT DOPAMINE TRANSPORTER (DA)-HOMO SAPENS (HUMAN), 620 aa.	0	5 (5p15.3)
589	cg46351913	1232	TCC/TGGGCTCTGT CGCTCTCTCTTC CCTGGGTACATG GCACAGAAC	T	C	Phe (818)	Ser (818)	NON- CONSER- ATIVE	transport	Human Gene SWISSPROT- ID:Q01959 SODIUM- DEPENDENT DOPAMINE TRANSPORTER (DA)-HOMO SAPENS (HUMAN), 620 aa.	0	5 (5p15.3)
590	cg43955093	4776	CTCGGTAGCTGT CCAGGCTCTGGIC IGICGGGGCCCT GTCATGTTGAG G	C	G	Ala (819)	Pro (819)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SPTRMEL- ACCO16084 P130 - HOMO SAPENS (HUMAN), 1139 aa.	0	16
591	cg43955093	522	GCATAGACATGG CGGCTTGGCC/C GICGAGAGCTG GGGGTACTCTA	C	G	Gly (820)	Arg (820)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP2694 HYPOTHICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
592	cg43958354	4604	CAACCCTAGAAG ACCTGGCTGCTTIV GAAAAGCTCTT CCAGACACAGTA	T	G	Leu (821)	Ile (821)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP46013 ANTIGEN KL-67 - Homo sapiens (Human), 3256 aa.	0	10 (1q25)

593	cg43070241	1841	CCATGGTACAGA CATCTACGTGTTIV GIGAAATGCCA AGCAAAATTGTCC	T	G	Phe (822)	Leu (822)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC:P51157 MICROSTYL- TRIGLYCERIDE TRANSFER PROTEIN, LARGE SUBUNIT PRECURSOR - Homo sapiens (Human), 894 aa.	0	4 (4q22)
594	cg43262121	2001	ACAAATTAGAGAG GGAGACTGACAI GTJIAACACCAGAT TGATCATGGTGCC AA	G	T	Gln (823)	Hs (823)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SPTRMEL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	
595	cg43262121	553	AATCGGAAGGT TTGGATCACTGGJA /TTCATCATGACC AGTGAGGAAGAG T	A	T	Ser (824)	Cys (824)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SPTRMEL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	
596	cg43262121	937	CCCCAAACAGGAA GTTCATGGCCJA /TJACCTGACAGC AGCTCTTAACCTC	A	T	Asn (825)	Tyr (825)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SPTRMEL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	
597	cg43262121	938	CCCAAACAGGAAAG TCCATGGGCCJA /TJCCCTGACAGCA GCTTCTTAACCTCC	A	T	Asn (826)	Ile (826)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SPTRMEL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	

598	cg44024279	301	CTGGAGAACCTT GCCATGAGAAAGI AAGAATTGAG AACTACGGACATT CA	A	G	Glu (827)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC-P02771 ALPHA- FETOPROTEIN PRECURSOR (ALPHA-FETOGLOBULIN) (ALPHA-1 FETOPROTEIN)- Homo sapiens (Human), 609 aa.	0
599	cg44928804	1235	AATGATTAACAAAC AACCTGAGAACACG AAGGGATGAAATG TTCGTGAAACACG T	G	A	Ala (828)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC-P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (FACTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTOGEN) - Homo sapiens (Human), 574 aa.	9, 1e-313 6 (6614)
600	cg43317253	367	GCCCCAGGATG GCTAGCTCTTG TJCGTGCAGGGA AGCTGGAGCTGG	G	T	Ala (829)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC-P21568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2.00E-301 9
601	cg44637661	223	CAGGTTCATCCA TTTTATTT(G/A) GACATCTGCTAG TGAAAGACCA	G	A	Gly (830)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC-O43913 ORIGIN RECOGNITION COMPLEX SUBUNIT 5 - Homo sapiens (Human), 435 aa.	6.10E-236
602	cg42913861	3034	CAGGTGTCTGG AGCCACCCGGG A/C/TCCGGGGGC GGGGGTGGCGGG GC	A	C	Ser (831)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACC-P09329 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3.00E-227 2 (2en)

603	cg4249389	526	AGAGGAGAGAGGCC GCCCTGAGGGGIA /GIGCAAAGCCATT GAGAAAAACTCA A	A	G	Ser (832)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene SWISSPROT- ACCP09471 GUANIN13 NUCLEOTIDE-BINDING PROTEIN G(O) ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.40E-188	15
604	cg41919239	335	GCCAGAGITGCAG CATCAGGGCCAGIA /CJGAUCAGAG ACCCCCAGTCCTA T	A	C	Ser (833)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACCP14207 PRECURSOR (PR-BETA) (FOLATE RECEPTOR, 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE- BINDING PROTEIN) (FBP)* Homo sapiens (Human), 255 aa.	4.20E-150	
605	cg4162952	787	TAGGAATGACAGC AGTAGCAGTAATIA /GIGGAAGGCCAA AAATCCCCCTGAG A	A	G	Arg (834)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACCP21583 STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT LIGAND) - Homo sapiens (Human), 273 aa.	3.70E-142	12

606	cg43945147	221	TGTTCTGGAGCCT CAATGGTACAGG/ CIGTCGTCGAAG GACAGTGTCAGTC	G	C	Arg (835)	Ser (835)	NON- CONSER- VATIVE	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC:P06337 LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR III-I PRECURSOR (FC-GAMMA RII) (FCR1) (IgG C RECEPTOR III-1) (FC-GAMMA RII-ALPHA) (CD16) (FCR-10)* Homo sapiens (Human), 254 aa.	1.60E-134	1
607	cg43926002	391	GGGCACAGAACAC CAGCACGGAGI CAGAGAACACA GACTGCCAACAG AT	C	S	Ser ???	Ser (836)	NON- CONSER- VATIVE	UNCLASSIFI- ED	Human Gene Homologous to SWISSPROT-ACC:P85639 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.60E-116	10
608	cg43972311	1609	ATTTGCCATTGTGGT AACTCTGGCTCTG TCACTATCTCGT GCCCAATTTGTG	T	G	Glu (837)	Ala (837)	NON- CONSER- VATIVE	UNCLASSIFI- ED	Human Gene Similar to TREM1 NEW-ACC:AA38008 GI YOYAJASE (EGC 4.4.1.5), HOMO SAPIENS (HUMAN), 184 aa.	2.20E-98	6
609	cg42556108	521	GTOAACGGGTGA TGGGACAGTA (A)CCTCAAACGAG CCAGGGGCTCCTT	C	A	Thr (838)	Asn (838)	NON- CONSER- VATIVE	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC:249913 ANTIBACTERIAL PROTEIN FALL-39 PRECURSOR (FALL-39 PEPTIDE ANTIBIOTIC) (ANTIMICROBIAL PROTEIN CAP18) (L1-37) - Homo sapiens (Human), 170 aa.	2.20E-87	3

610	gb3684290	487	AGTACTTCAGTA AACTCTGGGCTCA/ CIACTTCTGCACAA AAAGTACCTTGAG	A	C	Gln (839)	Pro (839)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to SWISSPROT-ACC-PO1282 VASSOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP)- Homo sapiens (HUMAN), 170 aa.	2.30E-85	
611	gb43942549	1032	CGGTATAACGCTA AAGATCCCTTTG/ TTTACGCCAAGCTT CAAAATTCTCTC	G	T	Val (840)	Phe (840)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to SPTREMBL-ACC-Q94218 CODED FOR BY C. ELEGANS CDNA CM1095 - CAENORHABDITIS ELEGANS, 589 aa.	2.80E-73	4
612	gb42381630	283	AAGGCGCTATGTA CAGCCTCTGAA/A /GTGATTGGCT ATGCGGCCCCGAGC A	A	G	Met (841)	Val (841)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to SPTREMBL-ACC-076087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
613	gb42381630	505	TGAGATGGCT GATGGCAGGAGI A/GTGACCCGCC AAAATCCAGAGAG GT	A	G	Met (842)	Val (842)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to SPTREMBL-ACC-076087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
614	gb304395	260	AATTCTGAAGGGT GGAGAACAGAGI GCTCTATCAA/AAA AAATATCTGCTCAT T	G	C	Gly (843)	Arg (843)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to SPTREMBL-ACC-G238693 T CELL RECEPTOR VARIABLE ALPHA CHAIN - HOMO SAPIENS (HUMAN), 143 aa (fragment).	1.00E-59	14 (14q11.2)

615	cg4396645	733	CACTCCCTCTCTT CTTGGATGCGAT TCACCCCTCCGTG GGGGCGAGATGG	A	T	Val (844)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to SWISSNEW-ACC-07670 GAMMA-SYNUCLEIN (PERSYN) (BREAST CANCER- SPECIFIC GENE 1 PROTEIN) Homo sapiens (Human), 127 aa.	1.20E-58
616	cg2526759	289	GAAGACAAGGGG TACAAAGGCCCTT AATCCTGGTGT CCACAGGGAGAC	T	A	Leu (845)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to RENTREMBL-ACC-G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54
617	cg2526759	342	TGTAACTCTCAATT GCAGTTAAGAAG ATGACTAACTTC GAAGCTCTATG	G	A	Val (846)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to RENTREMBL-ACC-G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54
618	cg2526759	364	GAAGTGACTAACT TTCGAAGCTACTT AATGGTACAGCA GGAAAAAGAACCT	T	A	Leu (847)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to RENTREMBL-ACC-G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54
619	cg2526759	475	AGCATATTAGATA AGAAAAGAACCTT /C/CACATCCGA ACATCACGCCAC	T	C	Pro (848)	NON- CONSER- ATIVE	UNCLASSIFI- ED	Human Gene Similar to RENTREMBL-ACC-G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54

620	cg40310734	1067	TACAAATAATTC GTCGGTCCCCGCG pCACTTGGAGCTG GACCTGGAGGG G	Gpp	C	Thr (849)	His (849)	FRAMES HIFT	cadherin	Human Gene SWISSPROT- ID: P08514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1IB) (INTEGRIN ALPHA-2 (IB) CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17421,3 2)
621	cg40310734	3285	GTGGGCTCTCAA GCGGAACCCGCG pAICAACCCCGAA GAAGATGATGAAG A	Gpp	A	Pro (850)	His (850)	FRAMES HIFT	cadherin	Human Gene SWISSPROT- ID: P08514 PLATELET MEMBRANE GLYCOPROTEIN IB PRECURSOR (GP1IB) (INTEGRIN ALPHA-2 (IB) CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17421,3 2)
622	cg43956660	2521	GTCCGACTCAC TTCACTATCTTG pCTAGTAGGAGGTG TATAGTCCTGTA	Gpp	Arg (851)	Glu (851)	Arg (851)	FRAMES HIFT	cadherin	Human Gene SWISSPROT- ID: Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa. alleles: SWISSPROT-ID: Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.	1.80E-157	

623	cg43970982	2429	CUCAGGATAGT TGACAGAAGGG ap/GIAGACCTGGC TAACCCAGAACCAAG CT	gap	G	Gly (852)	FRAMES HIFT	collagen	Human Gene SWISSPROT- ID:PI2111 COLLAGEN ALPHA- 3(V) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2	
624	cg42175288	1837	GCLATGGAGGCAA ATGGGGAGGAAGG ap/GIAAXACGACTAC AAGAAATGATCACGC GC	gap	G	Arg (853)	FRAMES HIFT	dna_mn_bind	Human Gene SWTPREMBL- ID:QP2804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17	
625	cg42175288	263	CGTTTACTCAGTT ATGGACAAGATG PCTATTCAGACTC CTATGTTGTTATG	gap	C	Tyr (854)	Leu (854)	FRAMES HIFT	dna_mn_bind	Human Gene SWTPREMBL- ID:QP2804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17
626	cg41534010	584	GGCCGAGCAGCTG CGGCCAGCTG ap/GIACCCCCCTAG CACAGCGCATGGA GA	gap	G	Thr (855)	Asp (855)	FRAMES HIFT	epith	Human Gene SWISSPROT- ID:R06727 APOLIPROTEIN A- IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa;SWISSPROT-ID:R06727 APOLIPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1,807-203	11 (11q23)
627	cg43065349	1353	CAGACTCTCAG Ap/GCTGTGATGAG ap/A[CGCGGGCTGC CTTGCCCAAGGGT A	gap	A	Thr (856)	Asn (856)	FRAMES HIFT	glycoprotein	Human Gene SWISSPROT- ID:P6452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2(P4.2) (PALLIDIN) -HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

628	cg41566531	999	TGACCAACGGGGTG CTGGATGCCCTCAGA pCTTATACTACATCCCT GGACCGGGGGGG A	gap	C	Leu (857)	FRAMES HIFT	glycoprotein	Human Gene Similar to ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.9E-70 (14q11.2)	14
629	cg41637704	1220	GCGCCGGCATGACA AGGGCACCGCAGCAG apGCCGCTGCAGA CTTGAAGGAACT GA	gap	G	Pro (858)	FRAMES HIFT	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEOROX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7
630	cg43933380	364	ATAAGTACAAATG CTTTTTTGTTTA/g AAA.....AAAAAA AAGTCCTACTTAA	gap	A	Leu (859)	FRAMES HIFT	interferon	Human Gene SWISSPROT- ID:P15260 INTERFERON- GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.40E-261	6
631	cg43072541	379	CCTGGGGCGCTGGT TCGTATCTGATTA/g pCJATCATTGATT ACGAAATAAACG T	gap	C	Ile (860)	FRAMES HIFT	kinase	Human Gene SWISSPROT- ID:Q15602 SERINE/TREONINE PROTEIN KINASE KIS-2 - HOMO SAPIENS (HUMAN), 487 aa.	9.6E-262	20

632	cg4032168	1336	GTCAGCCGCTTACCG TCGACTGTATCA P/TATGGGCCACATC AGAGACAAGGAAG C	gap	T	His	Leu (861)	FRAMES HIFT	protease	Human Gene Similar to SWISSPROT-ID:IP2135 COAGULATION FACTOR X (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.40E-82	2 (p413)
633	cg43931248	1317	CGGGCAGAGCTG CGTCGCGAGGCG ap/GCTCAAGTTAA AAGTGAGAGGCA CG	gap	G	Leu	Ala (862)	FRAMES HIFT	tgf	Human Gene SWISSPROT- ID:IP01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1)- HOMO SAPIENS (HUMAN), 390 aa.	9.70E-214	19
634	cg43931248	1317	CGGGCAGAGCTG CGTCGCGAGGCG ap/GCTCAAGTTAA AAGTGAGAGGCA CG	gap	G	Leu	Ala (863)	FRAMES HIFT	tgf	Human Gene SWISSPROT- ID:IP01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1)- HOMO SAPIENS (HUMAN), 390 aa.	9.70E-214	19
635	cg4372560	847	AATCCOCACACTG CAGGCCAGGGCG ap/CCTGGCCAGCTA CAAGAGAGGCTA CA	gap	C	Ala	Ala (864)	FRAMES HIFT	tgf receptor	Human Gene SWISSPROT- ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFBR-3) (BETAGLYCAN - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (p33)

636	cg43266471	1067	CCAGGATCATT GAGGATTAGG /TGTGCTGGACA CCATCAAACCTCTCA	gap	T	Gly (865)	FRAMES HIFT	tm7	Human Gene SWISSPROT- ID:173241 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR, PRECURSOR (VIP-R4) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP-R, TYPE II RECEPTOR) (PACAP-R- 2) (HOMO SAPIENS (HUMAN), 457 aa.)	5.20E-254	3
637	cg43995237	625	CAAATCCCCGTT TCCTCATCTG GACATGCTAAAT GAATAATCGACT	gap	G	Gln (866)	FRAMES HIFT	transferase	Human Gene SWISSPROT- ID:1752611 GERANYLGERANYL TRANSFERASE TYPE I BETA SUBUNIT (EC 2.4.1.-) (RAB GERANYLGERANYL TRANSFEE RASE BETA SUBUNIT) (RAB GERANYL- GERANYL TRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) • HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1

638	cg4395237	638	TCTCTAATCTGAC ATGGCTAAAGTGA G)AAATTACG TTTCCTCTATCAA	G	Leu (867)	FRAMES HIFT	transfase	Human Gene SWISSPROT- ID:P51611 (GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-)RAB GERANYLGERANYL TRANSFE- RASE BETA SUBUNIT) (RAB GERANYL- GERANYLTRANSFERASE BETA SUBUNIT) (RAB G6 TRANSFERASE) (RAB G6TASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	I	
639	cg4324094	267	CGGCCCTCTGCTGT GCTCTCTGCTG /GJGGTCCGCC AGCGCACTTC C	G	Arg (868)	FRAMES HIFT	UNCLASSIFI- D	Human Gene SWISSPROT- ACC-#P78539 SUSHI REPEAT- CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.40E-257	X	
640	cg44034555	665	ATCCAGGCTGAGC TGGATCATCTGAG /gap/GGCTCTAGC CACCCGTTTCCCT T	G	gap	Pro (869)	FRAMES HIFT	UNCLASSIFI- D	Human Gene SWISSPROT- ACC-Q13228 SELENIUM- BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.80E-252	I
641	cg44034555	667	CCAGGCTGAGCTG GATCATCTGAG /gap/CCCTCAOCCA CCGTTTCCCTG A	G	gap	Gly (870)	FRAMES HIFT	UNCLASSIFI- D	Human Gene SWISSPROT- ACC-Q13228 SELENIUM- BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.80E-252	I

642	cg39711096	882	AGCAGATGCCCG GGAGGCCACAG /gap/GTTACTCCCTC CAGCTGAGCACT GA	gap	G	Val (871)	FRAMES HIFT	UNCLASSIFI D	Human Gene SWISSPROT- ACCP18428 LIPOPOLYSACCHARIDE- BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
643	cg41428902	379	CGTCAGAGGAG CATATTCGCTGAA /gap/GACTCTGC AAGACTCATCCAG A	gap	C	Asp (872)	FRAMES HIFT	UNCLASSIFI D	Human Gene SWISSPROT- ACCP18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201	I (p36.2)
644	cg3946951	306	GGAACTCGAGCAC /TCGTCGGGGGAAAC /gap/CCCAAGATCA CGGGCCCTCTG GT	gap	Gly (873)	FRAMES HIFT	UNCLASSIFI D	Human Gene SWISSPROT- ACCP094467 FRUCTOSE-1,6'- BISPHOSPHATASE (EC 3.1.3.11) D-FRUCTOSE-1,6'- BISPHOSPHATE 1- PHOSPHOHYDROLASE (FBPASE) - Homo sapiens (Human), 337 aa.	3.50E-178	9 (q42.2)	
645	cg3948890	195	ATTCGGGGAG GGGGCCTGTAAG /gap/GAAAACACAGA CAATGCCATGAGA CT	gap	Pro (874)	Leu (874)	FRAMES HIFT	UNCLASSIFI D	Human Gene Homologous to SPRENBL-ACC-Q15182 SNRNP POLYPEPTIDE B * HOMO SAPIENS (HUMAN), 285 aa.	3.20E-147	20
646	cg3948890	197	TCCGGGGGGAGGG GCCCTGTAAGG /gap/AAACAGACA ATCCATGAGACT CC	gap	Phe (875)	Phe (875)	FRAMES HIFT	UNCLASSIFI D	Human Gene Homologous to SPRENBL-ACC-Q15182 SNRNP POLYPEPTIDE B * HOMO SAPIENS (HUMAN), 285 aa.	3.20E-147	20

647	cg43917524	713	GGGCCCTGTCGCC CAGTGAGGAGGI CtgtttCCGGCTGGT GTCTTAGGGGCA TC	C	Gpp	Ala	Pro (876)	FRAMES D HIFT	UNCLASSIFI E	Human Gene Homologous to TRIMBLINE-NEW-ACC-AD3025 PT10017 - HOMO SAPIENS (HUMAN), 258 aa.	3.20E-143	
648	cg43942004	373	CTCCTGGCACCTGGT GACTGCGAGA /gap/CTGGAGGG CTTCGGAGGGC TA	G	Asp	Glu (877)	FRAMES D HIFT	UNCLASSIFI E	Human Gene Homologous to SWISSNEW-ACC-Q9975 HEPARIN-BINDING EGFR-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERA TOXIN RECEPTOR) (DT-R) - Homo sapiens (human), 206 aa.	1.00E-107	5 (Sq33)	
649	cg43932428	681	TGTTGGCAGGTC CTCTCGGTAGIC /gap/CCCTTGCTCTG CCGACCTTGCTGG A	C	Gpp	Gly	Asp (878)	FRAMES D HIFT	UNCLASSIFI E	Human Gene Similar to SPTRM1B-ACC-06869 EDV-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.50E-72	
650	cg44010855	450	GGTCCAATGCCAA GTGCTCCCGGAAG /gap/GGACCCAGA TCGGTACAGGAA CG	G	Gpp	Gly	Asp (879)	FRAMES D HIFT	UNCLASSIFI E	Human Gene Similar to TRIMBLINE-ACC-AD18944 NIAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.80E-50	5
651	cg44010855	452	TCCAATGCCAAGT QCTCCCGGAAGG /gap/ACCCAGATC CGCTACAGGAGC TG	G	Gpp	Gly	Asp (880)	FRAMES D HIFT	UNCLASSIFI E	Human Gene Similar to TRIMBLINE-ACC-AD18944 NIAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.80E-50	5

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide selected from the group consisting of:
 - a) a nucleotide sequence comprising one or more polymorphic sequences
5 (SEQ ID NOS:1 - 651);
 - b) a fragment of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
 - c) a complementary nucleotide sequence comprising a sequence complementary to one or more of said polymorphic sequences (SEQ ID
10 NOS:1 - 651); and
 - d) a fragment of said complementary nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.
15
3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 100 nucleotides in length.
20
5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 90 nucleotides in length.

6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 75 nucleotides in length.
7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and
5 about 50 bases in length.
8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 40 bases in length.
- 10 9. The polynucleotide of claim 1, wherein said polynucleotide is derived from a nucleic acid encoding a polypeptide related to angiopoietin, 4-hydroxybutyrate dehydrogenase, ATP-dependent RNA helicase, MHC Class I histocompatibility antigen, or phosphoglycerate kinase.
- 15 10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1,
20 column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

5 14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:

a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 651) provided that the polymorphic sequence includes a 10 nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;

b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;

15 c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 651), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

20 d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize 25 under stringent conditions to a second polynucleotide selected from the group consisting of:

- a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 651), wherein said polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;
- 5 b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;
- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 651), wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and
- 10 d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and
15 about 51 bases in length.

17. The oligonucleotide of claim 15, wherein the oligonucleotide identifies a polypeptide related to angiopoietin, 4-hydroxybutyrate dehydrogenase, ATP-dependent RNA helicase, MHC Class I histocompatibility antigen, or phosphoglycerate kinase.

20 18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.

19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:

- 25 a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1 - 651, or its complement, provided that the polymorphic sequence

includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

- 5 b) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

10 20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

15 21. The method of claim 19, wherein said oligonucleotide identifies a polypeptide related to angiopoietin, 4-hydroxybutyrate dehydrogenase, ATP-dependent RNA helicase, MHC Class I histocompatibility antigen, or phosphoglycerate kinase.

20 22. The method of claim 19, wherein said oligonucleotide is between about 15 and about 30 bases in length.

25 23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a nucleic acid from said subject;
b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 651, or its complement, provided that the polymorphic sequence

includes a nucleotide other than the nucleotide recited in for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

c) determining whether said nucleic acid and said oligonucleotide hybridize;

5 whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.

24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:

10 a) providing a first nucleic acid and a second nucleic acid;

b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 651, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or 15 the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;

c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and

20 d) comparing hybridization of said first and second nucleic acids to said oligonucleotide,

wherein hybridization of the first and second nucleic acids to said oligonucleotide indicates the first and second nucleic acids are related.

25 25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement

of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

26. The method of claim 24, wherein the oligonucleotide is between about 10 and about
5 bases in length.
27. The method of claim 24, wherein the oligonucleotide is between about 10 and about
40 bases in length.
- 10 28. The method of claim 24, wherein the oligonucleotide is between about 15 and about
30 bases in length.
29. An isolated polypeptide comprising a polymorphic site at one or more amino acid
residues, wherein the protein is encoded by a polynucleotide selected from the group
consisting of: polymorphic sequences SEQ ID NOS:1 - 651, or their complement,
15 provided that the polymorphic sequence includes a nucleotide other than the
nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the
complement includes a nucleotide other than the complement of the nucleotide recited
in Table 1, column 5.
- 20 30. The polypeptide of claim 29, wherein said polypeptide is translated in the same open
reading frame as is a wild type protein whose amino acid sequence is identical to the
amino acid sequence of the polymorphic protein except at the site of the
polymorphism.
- 25 31. The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic
sequence, or its complement, includes the nucleotide listed in Table 2, column 6 or

Table 3, column 5 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 651, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.
33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising
- providing a protein sample from said subject;
 - contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and
 - detecting said antibody-antigen complexes,
- whereby the presence of said complexes indicates the presence of said polypeptide.

36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- 5 a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 651, or its complement; and
- 10 b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in a wild type allele of the sequence polymorphism,
- thereby treating said subject.

15 37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

20 38. A method of treating a subject suffering from, at risk for, or suspected of suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- 25 a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 651, or its complement; and
- 20 b) administering to the subject an effective therapeutic dose of a polypeptide,

wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 651, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 651, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, thereby treating said subject.

5 39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

10 a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 651, or its complement; and

15 b) administering to the subject an effective dose of the antibody of claim 34, thereby treating said subject.

20 40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

25 a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 651, or its complement; and

b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 651, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ

ID NOS:1 - 651, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence,

thereby treating said subject.

5 41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:

- a) a nucleotide sequence comprising one or more polymorphic sequences SEQ ID NOS:1 - 651;
- 10 b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences SEQ ID NOS:1 - 651; and
- 15 d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

20 42. The array of claim 41, wherein said array comprises 10 oligonucleotides.

43. The array of claim 41, wherein said array comprises at least 100 oligonucleotides.

44. The array of claim 41, wherein said array comprises at least 1000 oligonucleotides.

1/1

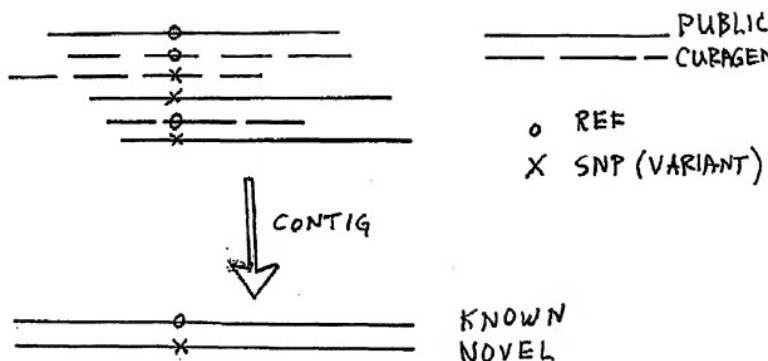


FIG. 1

SEQUENCE LISTING

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Shimkets, Richard A.
Leach, Martin D.

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CCATCTCCCTT CTGTGGCTGT CTCACGCAGA TGTATTTCGT TTTCATGTTC G

51

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51

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51

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51

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ACCAAGCTGCT CGTAGTACAC AGGCAAGCAC TTCTCCTTGC CTACCTCCAT G

51

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51

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51

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<400> 185
ACATCCAGGT GGTGTTGAC GCCGTTACCG ACATCATCAT TGCCAACAAC C

51

<210> 186
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CA GTGACGGC AGGGTCAAAG TCCTTAGCGT AGCCCTCGTT AAGGCTGTAG A

51

<210> 187
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AACCAGGCCA CTGTGAGAAG ACCACCGTGT TCAAGTCTTT GGGATGGCA G

51

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CCACAATGTT AGGAGGGTAT TTTTATATTCCTT CTCCAGTTAA CAAATACAGC A

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CTGCCCATCTT TCAGCCCTCT GAAACTGTGT CCAGCACAGA ATCTTCCCTG G

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GGCCTTCCCC GGTCCGGACA ATTGTCAGA CTATTGTCAA ACTGGGGAAT A

51

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51

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GGGAGGGTT TGTGTCCAAT ATCCCTTAAGG ACACGCAGGT GACTCGACAG G

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TCTTGGTGCAC TGAGTTGGGC TCTTCTAGAA CACCAGAGAC TGTGAGAATG G

51

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51

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51

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51

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GCCAATATAG GATAGGGCAC TACAGGTTCC GGTACAGTGA CACCCCTGGAG C

51

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51

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51

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51

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CGACGGAGGTG CTACGCGAGG GCGAGTTGGA GAAGCGCAGC GACAGCCTCT T

51

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TTTTTCCAG CTTACAATGG TACAGGCAGG AGCCTGGGGA AGGTCCCTGTC C

51

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AGAAGAGAGC CTGTGACACT GCCACTTGTG TGACTCATCG GCTGGCAGGC T 51

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<400> 207
TCATCCTGAG TTCTAAGAAG CTCCTCCTCA GTGACTCTGG CTTCTATCTC T 51

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AAGTCTGTGC TGATCCACAA GCCACGTGGG TGAGAGACGT GGTCAGGAGC A

51

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<221> misc_feature

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AGTTGAATC AGAGAGGAAT AAAAAGACA TTTTATATT TATTCTGCTC C

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TAAGCATGAG GTGGCACGAG GCAGGGGTG GCGATGCCAC CTGGGGGTCA C

51

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<400> 213
GGTCCCCTTG CTTTATCCA AGCTCTGAGG GACGCAGCCT GGCAATGGCTC T 51

<210> 214
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<210> 215
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<210> 216
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<210> 217
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51

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51

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AATCCACAAT CGGCATCAGG AAGCCCAAGT CCCAGTGGCC ATTAGGGTCC T

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CAACAGTTCC TTCAGCTTCC ATTTCACCCC TCATTTATCC CTCAACCCCC A 51

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TGCTCTCTT TCCCCTGCC CCAGAACTTT TATCCACTTA CCTAGATTCT A 51

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ACCGCACCT TTCCACCGGT GGGGGGCCCA GTGAAGTTA ACAAACTGCT G 51

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CATACCACGT TCACTGCAAG GGGGGAAACG TGTGGGTTGC TCTATTCAAG A 51

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GAAACCCAGT AGGCTCCTGG AGGCCCTGGT CAGCTTGCTT GGAATCCAGC A 51

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CACCTCCATC CCAGACAGGT CCCTCGCCTT CTCTGTGCAG TAGCATCAC T 51

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CGAGCGGCAC CCAGAGCTG CACCCGCCCT CACCGTCCTT CTGCGTCCCC C

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51

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51

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51

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CTTTCACITG GTGCTGGAGA ATTCAAGAGT CAAGAACATG CTAAGCATAA G

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51

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51

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<210> 345
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TCGGCAAATC TTGAAAGCTG CAGGGTGCGAG AGACATGGAT GTGACTTCCC A 51

<210> 346
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51

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51

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CAGCCGGGAG CTCTGCCAGC TTTGGTGAAAG GAGGGTGCTT GCCTCGTGCC C

51

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CGGGAGCTCT GCCAGCTTTG GCGAACGAGG GTGCTTGCTT CGTCCCCCTT G

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<210> 653
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Arg Leu His Arg Leu Arg Gly Glu Gln Met Ala Ser Tyr Phe
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<210> 667
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1 5 10

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<400> 676
Ser Ala Ser Lys Gln Ala Val Arg Pro Val Leu Ala Thr Thr
1 5 10

<210> 677
<211> 14
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<220>
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<400> 677
Tyr Cys Met Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu
1 5 10

<210> 678
<211> 14
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<400> 678
Val Gly Thr Tyr Arg Cys Val Pro Gly Lys Lys Gly Gly Tyr
1 5 10

<210> 679
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<400> 679
Gly Arg Ala Thr Ser Gly Ser Glu His Gln Phe Cys Gly
1 5 10

<210> 680
<211> 14
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<400> 680
Gly Glu Trp Ile Thr Val Asp Gln Thr Thr Ala Asn Arg
1 5 10

<210> 681
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<400> 681
Pro Glu Leu Val Leu Glu Leu Pro Ile Arg His Pro Lys Phe
1 5 10

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<223> cSNP translation

<400> 682

Glu	Trp	Phe	Lys	Asp	Leu	Ala	Leu	Lys	Trp	Tyr	Gly	Leu	Pro
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<210> 683

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<212> PRT

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<222> (7)...(0)

<223> cSNP translation

<400> 683

Tyr	Ile	Thr	Gly	Asp	Arg	Gly	Tyr	Met	Asp	Lys	Asp	Gly	Tyr
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<210> 684

<211> 14

<212> PRT

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<222> (7)...(0)

<223> cSNP translation

<400> 684

Ser	Gly	Tyr	Pro	Lys	Met	Ser	Ala	His	Thr	His	Ser	Ser	Phe
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<210> 685

<211> 14

<212> PRT

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<222> (7)...(0)

<223> cSNP translation

<400> 685

Val	Val	Lys	Ala	Phe	Val	Ile	Leu	Ala	Ser	Gln	Phe	Leu	Ser
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<210> 686

<211> 14

<212> PRT

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<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 686

Asp	Pro	Leu	Ile	Tyr	Ala	Phe	Arg	Ser	Gln	Glu	Met	Arg	Lys
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<210> 687

<211> 14

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<400> 687
Leu Ala Thr Leu Pro Glu Tyr Val Val Tyr Lys Pro Gln Met
1 5 10

<210> 688
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<400> 688
Leu Ala Pro Gln Gln Arg Val Ala Pro Gln Gln Lys Arg Ser
1 5 10

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<400> 689
Leu Tyr Arg Asp Ile Phe Glu His Leu Arg Asp Glu Ser Gly
1 5 10

<210> 690
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<400> 690
Asp Phe Tyr Tyr Leu Gly Ala Phe Phe Gly Gly Ser Val Gln
1 5 10

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 1 5 10

<210> 692
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<400> 692
 Arg Ala Leu Tyr Leu Leu Ile Arg Arg Val Leu His Leu Gly
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<210> 693
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<400> 693
 Glu Glu Ala Met Asn Ala Val Tyr Ser Gly Tyr Val Tyr Thr
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<210> 694
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<400> 694
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<210> 695
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<400> 695
 Glu Ser Thr Thr Val Gly Ser Ser
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<400> 696
Gln Gln Trp Ser Glu His His Ala Phe Leu Ser Gln Gly Ser
1 5 10

<210> 697
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<212> PRT
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<400> 697
Asp Asn Phe Ser Val Thr Glu Val Pro Phe Thr Glu Ser Ala
1 5 10

<210> 698
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<400> 698
Pro Gly Arg Arg Gln Arg Leu Thr Met Ala Ile Arg Thr Val
1 5 10

<210> 699
<211> 14
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<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 699
Leu Ala Gly Lys Val Ala Gln Val Lys Lys Asn Gly Arg Ile
1 5 10

<210> 700
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<400> 700
Leu Glu Asn Gln Lys Lys Val Arg Lys Lys Lys Val Leu Ile

1 5 10

<210> 701
<211> 14
<212> PRT
<213> Homo sapiens

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<400> 701
Val Ser Asp Glu Glu Leu Asp Gln Met Leu Asp Ser Gly Gln
1 5 10

<210> 702
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<400> 702
Trp Leu Gly Phe Asn Lys Gln Arg Gly His Leu Gln Ile Ala
1 5 10

<210> 703
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<400> 703
Glu Pro Glu Cys Arg Glu Val Phe His Arg Arg Ala Arg Ala
1 5 10

<210> 704
<211> 14
<212> PRT
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<220>
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<400> 704
Leu Pro Cys Gly Pro Gly Val Lys Gly Arg Cys Phe Gly Pro
1 5 10

<210> 705
<211> 14
<212> PRT
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<220>

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<223> cSNP translation

<400> 705
Ser Ala Met Asp Thr Arg Leu Leu Cys Cys Ala Val Ile Cys
1 5 10

<210> 706
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 706
Asn Thr Arg Leu Leu Cys His Val Met Leu Cys Leu Leu Gly
1 5 10

<210> 707
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<400> 707
Gln Thr Gly Asp Ser Ala Ile Tyr Leu Cys Ala Val Glu Ala
1 5 10

<210> 708
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<400> 708
Val Tyr Leu Cys Ala Val Asp Ala Tyr Ser Asn Asp Tyr Lys
1 5 10

<210> 709
<211> 14
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<400> 709
Gln Lys Gln Met Glu Leu Asp Ser Ile Leu Val Ala Leu Leu
1 5 10

<210> 710
<211> 14
<212> PRT
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<220>
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<400> 710
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1 5 10

<210> 711
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<400> 711
Pro Val Met Gly Leu Met Ile Tyr Met Met Val Met Asp His
1 5 10

<210> 712
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<400> 712
Ser Ser Gln Asp Pro Ala Ser Val Arg Glu Cys His Asp Pro
1 5 10

<210> 713
<211> 14
<212> PRT
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<400> 713
Val Leu Leu Leu Leu Gly Ala Cys Ala Ala Pro Pro Ala Trp
1 5 10

<210> 714
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<223> cSNP translation

<400> 714
Ser Leu Pro Tyr Ala Val Ala Pro Leu Ser Leu Pro Arg Gly
1 5 10

<210> 715

<211> 14

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<222> (7)...(0)

<223> cSNP translation

<400> 715

Tyr Gly Pro Gln Cys Gln Leu Val Ile Gln Cys Glu Pro Leu
1 5 10

<210> 716

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<223> cSNP translation

<400> 716

Thr Met Asp Cys Thr His Ser Leu Gly Asn Phe Ser Phe Ser
1 5 10

<210> 717

<211> 14

<212> PRT

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<223> cSNP translation

<400> 717

Gly Thr Thr Glu Thr Gly Gly Gln Gly Lys Gly Thr Ser Lys
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<210> 718

<211> 14

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<222> (7)...(0)

<223> cSNP translation

<400> 718

Cys Asn Gly Val Ala Val Cys Ser Asn Gln Asp Leu Ile Thr
1 5 10

<210> 719

<211> 14

<212> PRT

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<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 719

Leu Val Ser Tyr Cys Pro Arg Arg Leu Gln Gln Leu Leu Pro
1 5 10

<210> 720

<211> 14

<212> PRT

<213> Homo sapiens

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<222> (7)...(0)

<223> cSNP translation

<400> 720

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<210> 721

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 721

Tyr Ala Glu Arg Tyr Gln Met Pro Thr Gly Ile Lys Gly Pro
1 5 10

<210> 722

<211> 14

<212> PRT

<213> Homo sapiens

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<222> (7)...(0)

<223> cSNP translation

<400> 722

Asn Pro Leu Val Pro Gly Thr Pro Gly Arg Pro Gly Ile Pro
1 5 10

<210> 723

<211> 14

<212> PRT

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<400> 723
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1 5 10

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<400> 724
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1 5 10

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<400> 725
Gly Gly Gln Pro Cys Thr Ala Pro Leu Val Ala Phe Gln Pro
1 5 10

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<400> 726
Ser Pro Arg Ile Ser Ser Pro Arg Pro Gln Gly Leu Ser Asn
1 5 10

<210> 727
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<400> 727
Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1 5 10

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<222> (7)...(0)
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<400> 728
Ile Asn Ala Tyr Ile Ser His Leu Gly Phe Arg Phe
1 5 10

<210> 729
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 729
Leu His Ser Gly His Arg Gln Arg Pro Glu Phe Arg Pro Tyr
1 5 10

<210> 730
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<212> PRT
<213> Homo sapiens

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<400> 730
Cys Ser Gln Glu Ala Lys Gln Ser Ala Tyr Cys Pro Tyr Ser
1 5 10

<210> 731
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<222> (7)...(0)
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<400> 731
Arg Thr Ile Leu Ile Phe Gly Arg Cys Gln Glu Gln Phe Gly
1 5 10

<210> 732
<211> 14
<212> PRT
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<220>
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<223> cSNP translation

<400> 732
Asn Ala Asp Ile Ile Glu Ala Leu Arg Lys Lys Gly Phe Lys

1 5 10

<210> 733
<211> 9
<212> PRT
<213> Homo sapiens

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<400> 733
Asp Arg Val Glu Asn Tyr Lys Pro Arg
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<220>
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<222> (7)...(0)
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<400> 734
Ile Gln Thr Ala Glu Leu Thr Pro Glu Leu Val Ile Ser Asn
1 5 10

<210> 735
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
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<400> 735
Glu Gln Gln Gln Glu Gln His Gln Glu Gln Gln Glu Gln
1 5 10

<210> 736
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 736
Leu Ser Phe Ile Ser Thr Glu Leu Lys Tyr Pro Gly Met Pro
1 5 10

<210> 737
<211> 14
<212> PRT
<213> Homo sapiens

<220>

<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 737
Ile Leu Pro Ser Gly Leu Ala Phe Ile Ser Thr Gly Leu Lys
1 5 10

<210> 738
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 738
Phe Tyr Leu Ala Met Asn Glu Glu Gly Lys Leu Tyr Ala Lys
1 5 10

<210> 739
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 739
Gly Leu Asp Gln Lys Arg Ile Lys Tyr Val Val Gly Glu Leu
1 5 10

<210> 740
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<220>
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<400> 740
Ala Gly Leu Gly Gln Val Arg Leu Ile Val Gly Ile Leu Leu
1 5 10

<210> 741
<211> 14
<212> PRT
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<220>
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<400> 741
Thr Leu Thr Ser Val Gly His Gln Ser Val Thr Pro Gly Glu
1 5 10

<210> 742
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<212> PRT
<213> Homo sapiens

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<222> (7)...(0)
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<400> 742
Gly Gln Lys Thr Leu Thr Pro Val Gly Tyr Gln Ser Val Thr
1 5 10

<210> 743
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<400> 743
Thr Glu Ile Thr Gly Ala Thr Thr Met Thr Ser Val Gly His
1 5 10

<210> 744
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<220>
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<223> cSNP translation

<400> 744
Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln Tyr Asp Thr
1 5 10

<210> 745
<211> 14
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<213> Homo sapiens

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<222> (7)...(0)
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<400> 745
Pro Leu Ser Phe His Val Ile Trp Ile Ala Ser Phe Tyr Asn
1 5 10

<210> 746
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
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<400> 746
Ser Thr Ile Val Phe Leu Cys Pro Trp Ser Arg Gly Asn Phe
1 5 10

<210> 747
<211> 13
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 747
Pro Asp Pro Arg Glu Ala Cys Gly Ser Ser Ser Tyr Val
1 5 10

<210> 748
<211> 14
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<220>
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<400> 748
Ala Lys Asp Met Asn Gly Thr Ser Leu His Gly Lys Ala Ile
1 5 10

<210> 749
<211> 14
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<213> Homo sapiens

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<400> 749
Arg Ser Ala Arg Gly Ser Arg Gly Gly Thr Arg Gly Trp Leu
1 5 10

<210> 750
<211> 14
<212> PRT
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<220>
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<222> (7)...(0)
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<400> 750
Asn Phe Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser
1 5 10

<210> 751

<211> 14
<212> PRT
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<400> 751
Ile Gln Tyr Thr Tyr Leu Gly Gly His Val Cys Leu Ser Ala
1 5 10

<211> 752
<212> 14
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<222> (7)...(0)
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<400> 752
Leu Asp Pro Asn Asn Pro Asp Ala Asn Trp Ile His Ala Arg
1 5 10

<211> 753
<212> 14
<213> PRT
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<220>
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<222> (7)...(0)
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<400> 753
Cys Leu Thr Glu Arg Gln Ser Lys Ile Trp Phe Gln Asn Arg
1 5 10

<211> 754
<212> 14
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<220>
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<222> (7)...(0)
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<400> 754
Pro Tyr Arg Ile Ala His Ala Val Ile Lys Ala His Ala Arg
1 5 10

<211> 755
<212> 14
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<220>
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<400> 755
Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser
1 5 10

<210> 756
<211> 14
<212> PRT
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<222> (7)...(0)
<223> cSNP translation

<400> 756
Ile Lys Asn Glu Ala Arg Leu Pro Cys Leu Pro Thr Pro Gly
1 5 10

<210> 757
<211> 14
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<222> (7)...(0)
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<400> 757
Ala Arg Lys Phe Phe Glu Asn Leu Pro Asp Gly Thr Trp Asn
1 5 10

<210> 758
<211> 8
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
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<400> 758
Phe Ser Tyr Ser Ala Ser Ser Thr
1 5

<210> 759
<211> 14
<212> PRT
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<222> (7)...(0)
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<400> 759
Pro Val Ser Ser Ala Asn Val Met Ser Gly Ile Ser Ser Val
1 5 10

<210> 760
<211> 14
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<213> Homo sapiens

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<222> (7)...(0)

<223> cSNP translation

<400> 760

Trp Glu Arg Phe Val His Arg Glu Asn Gln His Leu Val Ser
1 5 10

<210> 761

<211> 14

<212> PRT

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<400> 761

Gly Thr Glu Asp Leu Tyr Gly Tyr Ile Asp Lys Tyr Asn Ile
1 5 10

<210> 762

<211> 14

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<400> 762

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Leu Tyr Ser Arg Leu Gly Gly Gln Pro Val Tyr Leu Pro Thr
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Ala Pro Pro Gly Ala Tyr His Gly Ala Pro Gly Ala Tyr Pro
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Val Met Pro His Ser Ser Glu His Lys Thr Ala Gln Pro Asn
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Thr Cys Val Val Glu His Thr Gly Ala Pro Glu Pro Ile Leu
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<220>
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<222> (7)...(0)

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<213> Homo sapiens

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<210> 827

<211> 14

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<211> 14

<212> PRT

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<210> 829
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Gly Met Ala Ser Ser Cys Ser Val Gln Val Lys Leu Glu Leu
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<210> 830
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<400> 830
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1 5 10

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Pro Pro Pro Pro Pro Gly Ala Pro Gly Gly Ser Gln Asp Thr
1 5 10

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1 5 10

<210> 833
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<400> 833
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1 5 10

<210> 836
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1 5 10

<210> 837
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<400> 837
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<210> 838
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<400> 838
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1 5 10

<210> 839
<211> 14
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1 5 10

<210> 840
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1 5 10

<210> 841
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<212> PRT
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<210> 842
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<400> 842
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<210> 843
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<400> 843
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1 5 10

<210> 844
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<400> 845
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1 5 10

<210> 846
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<400> 846
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1 5 10

<210> 847

<211> 14
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<400> 847
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1 5 10

<210> 848
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<400> 848
Leu Asp Lys Lys Glu Leu Ser Ser Ile Leu Asn Ile Thr Ala
1 5 10

<210> 849
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<400> 849
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1 5 10

<210> 850
<211> 14
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<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 850
Phe Phe Lys Arg Asn Arg His Thr Pro Gly Arg Arg
1 5 10

<210> 851
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
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<223> cSNP translation

<400> 851
Thr Ile Gln Pro Pro Arg Glu
1 5

<210> 852
<211> 14
<212> PRT
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<220>
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<222> (8)...(0)
<223> cSNP translation

<400> 852
Gly Ile Val Gly Gln Lys Gly Arg Pro Trp Leu Pro Arg Thr
1 5 10

<210> 853
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (8)...(0)
<223> cSNP translation

<400> 853
Gly Gly Lys Met Gly Gly Arg Lys Arg Leu Gln Lys
1 5 10

<210> 854
<211> 14
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<213> Homo sapiens

<220>
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<400> 854
Tyr Ser Ser Tyr Gly Gln Ser Leu Phe Thr Val Leu Trp Trp
1 5 10

<210> 855
<211> 14
<212> PRT
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<220>
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<222> (8)...(0)
<223> cSNP translation

<400> 855
Glu Gln Leu Arg Arg Gln Leu Asp Pro Leu Arg Thr Ala His
1 5 10

<210> 856
<211> 14
<212> PRT

<213> Homo sapiens

<220>

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<223> cSNP translation

<400> 856

Ser Thr Glu Cys Trp Met Asn Ala Ala Cys Leu Ala Pro Gly
1 5 10

<210> 857

<211> 14

<212> PRT

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<223> cSNP translation

<400> 857

His Gly Val Leu Asp Ala Cys Leu Ile His Pro Gly Pro Ala
1 5 10

<210> 858

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<223> cSNP translation

<400> 858

Arg Asp Lys Gly Ser Gly Arg Ala Cys Gly Leu Glu Gly Gln
1 5 10

<210> 859

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 859

Thr Asp Phe Phe Phe Phe
1 5

<210> 860

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (8)...(0)

<223> cSNP translation

<400> 860

Gly Ala Gly Ser Val Ser Asp His His Ser Ile Thr Lys
1 5 10

<210> 861
<211> 12
<212> PRT
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<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 861
Arg Tyr Leu Asp Trp Ile Leu Trp Ala His Gln Arg
1 5 10

<210> 862
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<212> PRT
<213> Homo sapiens

<220>
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<223> cSNP translation

<400> 862
Ala Glu Leu Arg Leu Leu Arg Ala Gln Val Lys Ser Gly Ala
1 5 10

<210> 863
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<223> cSNP translation

<400> 863
Ala Glu Leu Arg Leu Leu Arg Ala Gln Val Lys Ser Gly Ala
1 5 10

<210> 864
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<223> cSNP translation

<400> 864
Pro His Cys Arg Pro Gly Ala Trp Pro Ala Thr Glu Arg Gly
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<210> 865
<211> 14
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<220>

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<222> (8)...(0)

<223> cSNP translation

<400> 865

Ile His Phe Glu Asp Tyr Gly Val Leu Gly His His Gln Leu
1 5 10

<210> 866

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<212> PRT

<213> Homo sapiens

<220>

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<223> cSNP translation

<400> 866

Asn Phe Ile Leu Ala Cys Pro Arg
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<210> 867

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 867

Arg Glu Lys Leu Arg Asn Phe His Ser Phe Ser Met Ser Arg
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<210> 868

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (8)...(0)

<223> cSNP translation

<400> 868

Leu Leu Leu Leu Leu Arg Arg Pro Ala Gln Pro Gln Leu
1 5 10

<210> 869

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

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<223> cSNP translation

<400> 869

Lys Arg Val Ala Gly Gly Leu Arg
1 5

<210> 870
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<212> PRT
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<220>
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<223> cSNP translation

<400> 870
Gly Lys Arg Val Ala Gly Gly Leu Arg
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<210> 871
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<212> PRT
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<220>
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<223> cSNP translation

<400> 871
Ser Ser Gly Arg Pro Thr Gly Tyr Cys Leu Gln Leu Gln Gln
1 5 10

<210> 872
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (8)...(0)
<223> cSNP translation

<400> 872
Gln Arg Ser Ile Ser Ala Asp
1 5

<210> 873
<211> 14
<212> PRT
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<220>
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<222> (8)...(0)
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<400> 873
Arg Ala Pro Val Ile Leu Gly Pro Pro Thr Thr Cys Ser Ser
1 5 10

<210> 874
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 874
Met Gly Leu Ser Gly Phe Leu Thr Gly Pro Pro Pro Pro Gly
1 5 10

<210> 875
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (8)...(0)
<223> cSNP translation

<400> 875
Leu Met Gly Leu Ser Gly Phe Leu Thr Gly Pro Pro Pro Pro
1 5 10

<210> 876
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 876
Pro Arg Thr Pro Ala Glu Pro Pro Pro Leu Gly Arg Gln Ala
1 5 10

<210> 877
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (7)...(0)
<223> cSNP translation

<400> 877
Gly Thr Gly Asp Trp Arg Glu Pro Gly Ala Ala Ser Glu Arg
1 5 10

<210> 878
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<213> Homo sapiens

<220>
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<222> (9)...(0)
<223> cSNP translation

<400> 878
Gln Gly Arg Gln Ser Lys Gly Leu Arg Arg Arg Thr Trp Pro
1 5 10

<210> 879

<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (8)...(0)
<223> cSNP translation

<400> 879
Lys Cys Lys Cys Ser Arg Lys Asp Pro Arg Ser Ala Thr Ala
1 5 10

<211> 880
<212> 14
<213> PRT
<213> Homo sapiens

<220>
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<222> (7)...(0)
<223> cSNP translation

<400> 880
Cys Lys Cys Ser Arg Lys Asp Pro Arg Ser Ala Thr Ala Thr
1 5 10

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